Figure 1

Human
Glial Cell Line-Derived
Neurotrophic Factor Receptor Protein

```
          10                                  30                                  50
AATCTGGCCTCGGAACACGCCATTCTCCGCGCCGCTTCCAATAACCACTAACATCCCTA

          70                                  90                                  110
ACGAGCATCCGAGCCGAGGGCTCTGCTCGGAAATCGTCCTGGCCCAACTCGGCCCTTCGA

          130                                 150                                 170
GCTCTCGAAGATTACCGCATCTATTTTTTTTTCTTTTTTTTCTTTTCCTAGCGCAGATA

          190                                 210                                 230
AAGTGAGCCCGGAAAGGGAAGGAGGGGGCGGGGACACCATTGCCCTGAAAGAATAAATAA

          250                                 270                                 290
GTAAATAAACAAACTGGCTCCTCGCCGCAGCTGGACGCGGTCGGTTGAGTCCAGGTTGGG

          310                                 330                                 350
TCGGACCTGAACCCCTAAAAGCGGAACCGCCTCCCGCCCTCGCCATCCCGGAGCTGAGTC

          370                                 390                                 410
GCCGGCGGCGGTGGCTGCTGCCAGACCCGGAGTTTCCTCTTTCACTGGATGGAGCTGAAC

          430                                 450                                 470
TTTGGGCGGCCAGAGCAGCACAGCTGTCCGGGGATCGCTGCACGCTGAGCTCCCTCGGCA

          490                                 510                                 530
AGACCCAGCGGCGGCTCGGGATTTTTTTGGGGGGGCGGGGACCAGCCCCGCGCCGGCACC

          550                                 570                                 590
ATGTTCCTGGCGACCCTGTACTTCGCGCTGCCGCTCTTGGACTTGCTCCTGTCGGCCGAA
M  F  L  A  T  L  Y  F  A  L  P  L  L  D  L  L  L  S  A  E
```

Figure 1 (continued)

```
        610                         630                         650
GTGAGCGGCGGAGACCGCCTGGATTGCGTGAAAGCCAGTGATCAGTGCCTGAAGGAGCAG
V  S  G  G  D  R  L  D  C  V  K  A  S  D  Q  C  L  K  E  Q

        670                         690                         710
AGCTGCAGCACCAAGTACCGCACGCTAAGGCAGTGCGTGGCGGGCAAGGAGACCAACTTC
S  C  S  T  K  Y  R  T  L  R  Q  C  V  A  G  K  E  T  N  F

        730                         750                         770
AGCCTGGCATCCGGCCTGGAGGCCAAGGATGAGTGCCGCAGCGCCATGGAGGCCCTGAAG
S  L  A  S  G  L  E  A  K  D  E  C  R  S  A  M  E  A  L  K

        790                         810                         830
CAGAAGTCGCTCTACAACTGCCGCTGCAAGCGGGGTATGAAGAAGGAGAAGAACTGCCTG
Q  K  S  L  Y  N  C  R  C  K  R  G  M  K  K  E  K  N  C  L

        850                         870                         890
CGCATTTACTGGAGCATGTACCAGAGCCTGCAGGGAAATGATCTGCTGGAGGATTCCCCA
R  I  Y  W  S  M  Y  Q  S  L  Q  G  N  D  L  L  E  D  S  P

        910                         930                         950
TATGAACCAGTTAACAGCAGATTGTCAGATATATTCCGGGTGGTCCCATTCATATCAGAT
Y  E  P  V  N  S  R  L  S  D  I  F  R  V  V  P  F  I  S  D

        970                         990                        1010
GTTTTTCAGCAAGTGGAGCACATTCCCAAAGGGAACAACTGCCTGGATGCAGCGAAGGCC
V  F  Q  Q  V  E  H  I  P  K  G  N  N  C  L  D  A  A  K  A

       1030                        1050                        1070
TGCAACCTCGACGACATTTGCAAGAAGTACAGGTCGGCGTACATCACCCCGTGCACCACC
C  N  L  D  D  I  C  K  K  Y  R  S  A  Y  I  T  P  C  T  T

       1090                        1110                        1130
AGCGTGTCCAACGATGTCTGCAACCGCCGCAAGTGCCACAAGGCCCTCCGGCAGTTCTTT
S  V  S  N  D  V  C  N  R  R  K  C  H  K  A  L  R  Q  F  F
```

Figure 1 (continued)

1150 1170 1190

GACAAGGTCCCGGCCAAGCACAGCTACGGAATGCTCTTCTGCTCCTGCCGGGACATCGCC

D K V P A K H S Y G M L F C S C R D I A

1210 1230 1250

TGCACAGAGCGGAGGCGACAGACCATCGTGCCTGTGTGCTCCTATGAAGAGAGGGAGAAG

C T E R R R Q T I V P V C S Y E E R E K

1270 1290 1310

CCCAACTGTTTGAATTTGCAGGACTCCTGCAAGACGAATTACATCTGCAGATCTCGCCTT

P N C L N L Q D S C K T N Y I C R S R L

1330 1350 1370

GCGGATTTTTTTACCAACTGCCAGCCAGAGTCAAGGTCTGTCAGCAGCTGTCTAAAGGAA

A D F F T N C Q P E S R S V S S C L K E

1390 1410 1430

AACTACGCTGACTGCCTCCTCGCCTACTCGGGGCTTATTGGCACAGTCATGACCCCCAAC

N Y A D C L L A Y S G L I G T V M T P N

1450 1470 1490

TACATAGACTCCAGTAGCCTCAGTGTGGCCCCATGGTGTGACTGCAGCAACAGTGGGAAC

Y I D S S S L S V A P W C D C S N S G N

1510 1530 1550

GACCTAGAAGAGTGCTTGAAATTTTTGAATTTCTTCAAGGACAATACATGTCTTAAAAAT

D L E E C L K F L N F F K D N T C L K N

1570 1590 1610

GCAATTCAAGCCTTTGGCAATGGCTCCGATGTGACCGTGTGGCAGCCAGCCTTCCCAGTA

A I Q A F G N G S D V T V W Q P A F P V

1630 1650 1670

CAGACCACCACTGCCACTACCACCACTGCCCTCCGGGTTAAGAACAAGCCCCTGGGGCCA

Q T T T A T T T T A L R V K N K P L G P

Figure 1 (continued)

```
        1690                1710                1730
GCAGGGTCTGAGAATGAAATTCCCACTCATGTTTTGCCACCGTGTGCAAATTTACAGGCA
A   G   S   E   N   E   I   P   T   H   V   L   P   P   C   A   N   L   Q   A

        1750                1770                1790
CAGAAGCTGAAATCCAATGTGTCGGGCAATACACACCTCTGTATTTCCAATGGTAATTAT
Q   K   L   K   S   N   V   S   G   N   T   H   L   C   I   S   N   G   N   Y

        1810                1830                1850
GAAAAAGAAGGTCTCGGTGCTTCCAGCCACATAACCACAAAATCAATGGCTGCTCCTCCA
E   K   E   G   L   G   A   S   S   H   I   T   T   K   S   M   A   A   P   P

        1870                1890                1910
AGCTGTGGTCTGAGCCCACTGCTGGTCCTGGTGGTAACCGCTCTGTCCACCCTATTATCT
S   C   G   L   S   P   L   L   V   L   V   V   T   A   L   S   T   L   L   S

        1930                1950                1970
TTAACAGAAACATCATAGCTGCATTAAAAAAATACAATATGGACATGTAAAAAGACAAAA
L   T   E   T   S   *

        1990                2010                2030
ACCAAGTTATCTGTTTCCTGTTCTCTTGTATAGCTGAAATTCCAGTTTAGGAGCTCAGTT

        2050                2070                2090
GAGAAACAGTTCCATTCAACTGGAACATTTTTTTTTT.CCTTTTAAGAAAGCTTCTTGT

        2110                2130                2150
GATCCTT.GGGGCTTCTGTGAAAAACCTGATGCAGTGCTCCATCCAAACTCAGAAGGCTT

        2170                2190                2210
TGGGATATGCTGTATTTTAAAGGGACAGTTTGTAACTTGGGCTGTAAAGCAAACTGGGGC

        2230                2250                2270
TGTGTTTTCGATGATGATGAT.ATCATGAT.ATGAT........................

        2290                2310                2330
...............GATTTTAACAGTTTTACTTCTGGCCTTTCCTAGCTAGAGAAGGAG
```

Figure 1 (continued)

2350 2370 2390
TTAATATTTCTAAGGTAACTCCCATATCTCCTTTAATGACATTGATTTCTAATGATATAA

2410 2430 2450
ATTTCAGCCTACATTGATGCCAAGCTTTTTTGCCACAAAGAAGATTCTTACCAAGAGTGG

2470 2490 2510
GCTTTGTGGAAACAGCTGGTACTGATGTTCACCTTTATATATGTACTAGCATTTTCCACG

2530 2550
CTGATGTTTATGTACTGTAAACAGTTCTGCACTCTTGTACAAAAGAAAA

Note: The dots in the above sequence listing from 2240 to 2300 indicate positions of divergence between different receptor clones. One of the human clones contains an insert of 39 nucleotides from 2258 to 2297 and has different bases at positions 2244 and 2253.

Figure 2

Human
Glial Cell Line-Derived
Neurotrophic Factor Receptor Protein

M	F	L	A	T	L	Y	F	A	L	P	L	L	D	L	L	L	S	A	E	20
V	S	G	G	D	R	L	D	C	V	K	A	S	D	Q	C	L	K	E	Q	40
S	C	S	T	K	Y	R	T	L	R	Q	C	V	A	G	K	E	T	N	F	60
S	L	A	S	G	L	E	A	K	D	E	C	R	S	A	M	E	A	L	K	80
Q	K	S	L	Y	N	C	R	C	K	R	G	M	K	K	E	K	N	C	L	100
R	I	Y	W	S	M	Y	Q	S	L	Q	G	N	D	L	L	E	D	S	P	120
Y	E	P	V	N	S	R	L	S	D	I	F	R	V	V	P	F	I	S	D	140
V	F	Q	Q	V	E	H	I	P	K	G	N	N	C	L	D	A	A	K	A	160
C	N	L	D	D	I	C	K	K	Y	R	S	A	Y	I	T	P	C	T	T	180
S	V	S	N	D	V	C	N	R	R	K	C	H	K	A	L	R	Q	F	F	200
D	K	V	P	A	K	H	S	Y	G	M	L	F	C	S	C	R	D	I	A	220
C	T	E	R	R	R	Q	T	I	V	P	V	C	S	Y	E	E	R	E	K	240
P	N	C	L	N	L	Q	D	S	C	K	T	N	Y	I	C	R	S	R	L	260
A	D	F	F	T	N	C	Q	P	E	S	R	S	V	S	S	C	L	K	E	280
N	Y	A	D	C	L	L	A	Y	S	G	L	I	G	T	V	M	T	P	N	300
Y	I	D	S	S	S	L	S	V	A	P	W	C	D	C	S	N	S	G	N	320
D	L	E	E	C	L	K	F	L	N	F	F	K	D	N	T	C	L	K	N	340
A	I	Q	A	F	G	N	G	S	D	V	T	V	W	Q	P	A	F	P	V	360
Q	T	T	T	A	T	T	T	T	A	L	R	V	K	N	K	P	L	G	P	380
A	G	S	E	N	E	I	P	T	H	V	L	P	P	C	A	N	L	Q	A	400
Q	K	L	K	S	N	V	S	G	N	T	H	L	C	I	S	N	G	N	Y	420
E	K	E	G	L	G	A	S	S	H	I	T	T	K	S	M	A	A	P	P	440
S	C	G	L	S	P	L	L	V	L	V	V	T	A	L	S	T	L	L	S	460
L	T	E	T	S	*	465														

Figure 3

Rat
Glial Cell Line-Derived
Neurotrophic Factor Receptor Protein

```
       10                    30                   50
AGCTCGCTCTCCCGGGGCAGTGGTGTGGATGCACCGGAGTTCGGGCGCTGGGCAAGTTGG

       70                    90                   110
GTCGGAACTGAACCCCTGAAAGCGGGTCCGCCTCCCGCCCTCGCGCCCGCCCGGATCTGA

       130                   150                  170
GTCGCTGGCGGCGGTGGGCGGCAGAGCGACGGGGAGTCTGCTCTCACCCTGGATGGAGCT

       190                   210                  230
GAACTTTGAGTGGCCAGAGGAGCGCAGTCGCCCGGGGATCGCTGCACGCTGAGCTCTCTC

       250                   270                  290
CCCGAGACCGGGCGGCGGCTTTGGATTTTGGGGGGGCGGGGACCAGCTGCGCGGCGGCAC

       310                   330                  350
CATGTTCCTAGCCACTCTGTACTTCGCGCTGCCACTCCTGGATTTGCTGATGTCCGCCGA
 M  F  L  A  T  L  Y  F  A  L  P  L  L  D  L  L  M  S  A  E

       370                   390                  410
GGTGAGTGGTGGAGACCGTCTGGACTGTGTGAAAGCCAGCGATCAGTGCCTGAAGGAACA
 V  S  G  G  D  R  L  D  C  V  K  A  S  D  Q  C  L  K  E  Q

       430                   450                  470
GAGCTGCAGCACCAAGTACCGCACACTAAGGCAGTGCGTGGCGGGCAAGGAAACCAACTT
 S  C  S  T  K  Y  R  T  L  R  Q  C  V  A  G  K  E  T  N  F

       490                   510                  530
CAGCCTGACATCCGGCCTTGAGGCCAAGGATGAGTGCCGTAGCGCCATGGAGGCCTTGAA
 S  L  T  S  G  L  E  A  K  D  E  C  R  S  A  M  E  A  L  K
```

Figure 3 (continued)

550 570 590

GCAGAAGTCTCTGTACAACTGCCGCTGCAAGCGGGGCATGAAGAAAGAGAAGAATTGTCT

Q K S L Y N C R C K R G M K K E K N C L

610 630 650

GCGTATCTACTGGAGCATGTACCAGAGCCTGCAGGGAAATGACCTCCTGGAAGATTCCCC

R I Y W S M Y Q S L Q G N D L L E D S P

670 690 710

GTATGAGCCGGTTAACAGCAGGTTGTCAGATATATTCCGGGCAGTCCCGTTCATATCAGA

Y E P V N S R L S D I F R A V P F I S D

730 750 770

TGTTTTCCAGCAAGTGGAACACATTTCCAAAGGGAACAACTGCCTGGACGCAGCCAAGGC

V F Q Q V E H I S K G N N C L D A A K A

790 810 830

CTGCAACCTGGACGACACCTGTAAGAAGTACAGGTCGGCCTACATCACCCCCTGCACCAC

C N L D D T C K K Y R S A Y I T P C T T

850 870 890

CAGCATGTCCAACGAGGTCTGCAACCGCCGTAAGTGCCACAAGGCCCTCAGGCAGTTCTT

S M S N E V C N R R K C H K A L R Q F F

910 930 950

CGACAAGGTTCCGGCCAAGCACAGCTACGGGATGCTCTTCTGCTCCTGCCGGGACATCGC

D K V P A K H S Y G M L F C S C R D I A

970 990 1010

CTGCACCGAGCGGCGGCGACAGACTATCGTCCCCGTGTGCTCCTATGAAGAACGAGAGAG

C T E R R R Q T I V P V C S Y E E R E R

1030 1050 1070

GCCCAACTGCCTGAGTCTGCAAGACTCCTGCAAGACCAATTACATCTGCAGATCTCGCCT

P N C L S L Q D S C K T N Y I C R S R L

Figure 3 (continued)

1090 1110 1130

TGCAGATTTTTTTACCAACTGCCAGCCAGAGTCAAGGTCTGTCAGCAACTGTCTTAAGGA

A D F F T N C Q P E S R S V S N C L K E

1150 1170 1190

GAACTACGCAGACTGCCTCCTGGCCTACTCGGGACTGATTGGCACAGTCATGACTCCCAA

N Y A D C L L A Y S G L I G T V M T P N

1210 1230 1250

CTACGTAGACTCCAGCAGCCTCAGCGTGGCACCATGGTGTGACTGCAGCAACAGCGGCAA

Y V D S S S L S V A P W C D C S N S G N

1270 1290 1310

TGACCTGGAAGACTGCTTGAAATTTCTGAATTTTTTTAAGGACAATACTTGTCTCAAAAA

D L E D C L K F L N F F K D N T C L K N

1330 1350 1370

TGCAATTCAAGCCTTTGGCAATGGCTCAGATGTGACCATGTGGCAGCCAGCCCCTCCAGT

A I Q A F G N G S D V T M W Q P A P P V

1390 1410 1430

CCAGACCACCACTGCCACCACTACCACTGCCTTCCGGGTCAAGAACAAGCCTCTGGGGCC

Q T T T A T T T T A F R V K N K P L G P

1450 1470 1490

AGCAGGGTCTGAGAATGAGATCCCCACACACGTTTTACCACCCTGTGCGAATTTGCAGGC

A G S E N E I P T H V L P P C A N L Q A

1510 1530 1550

TCAGAAGCTGAAATCCAATGTGTCGGGTAGCACACACCTCTGTCTTTCTGATAGTGATTT

Q K L K S N V S G S T H L C L S D S D F

1570 1590 1610

CGGAAAGGATGGTCTCGCTGGTGCCTCCAGCCACATAACCACAAAATCAATGGCTGCTCC

G K D G L A G A S S H I T T K S M A A P

Figure 3 (continued)

1630 1650 1670

TCCCAGCTGCAGTCTGAGCTCACTGCCGGTGCTGATGCTCACCGCCCTTGCTGCCCTGTT

P S C S L S S L P V L M L T A L A A L L

1690 1710 1730

ATCTGTATCGTTGGCAGAAACGTCGTAGCTGCATCCGGGAAAACAGTATGAAAAGACAAA

S V S L A E T S *

1750 1770 1790

AGAGAACCAAGTATTCTGTCCCTGTCCTCTTGTATATCTGAAAATCCAGTTTTAAAAGCT

1810 1830 1850

CCGTTGAGAAGCAGTTTCACCCAACTGGAACTCTTTCCTTGTTTTTAAGAAAGCTTGTGG

1870 1890 1910

CCCTCAGGGGCTTCTGTTGAAGAACTGCTACAGGGCTAATTCCAAACCCATAAGGCTCTG

1930 1950 1970

GGGCGTGGTGCGGCTTAAGGGGACCATTTGCACCATGTAAAGCAAGCTGGGCTTATCATG

1990 2010 2030

TGTTTGATGGTGAGGATGGTAGTGGTGATGATGATGGTAATTTTAACAGCTTGAACCCTG

2050 2070 2090

TTCTCTCTACTGGTTAGGAACAGGAGATACTATTGATAAAGATTCTTCCATGTCTTACTC

2110 2130

AGCAGCATTGCCTTCTGAAGACAGGCCCGCAGCCGTCG

Figure 4

Rat
Glial Cell Line-Derived
Neurotrophic Factor Receptor Protein

```
M F L A T L Y F A L P L L D L L M S A E  20
V S G G D R L D C V K A S D Q C L K E Q  40
S C S T K Y R T L R Q C V A G K E T N F  60
S L T S G L E A K D E C R S A M E A L K  80
Q K S L Y N C R C K R G M K K E K N C L 100
R I Y W S M Y Q S L Q G N D L L E D S P 120
Y E P V N S R L S D I F R A V P F I S D 140
V F Q Q V E H I S K G N N C L D A A K A 160
C N L D D T C K K Y R S A Y I T P C T T 180
S M S N E V C N R R K C H K A L R Q F F 200
D K V P A K H S Y G M L F C S C R D I A 220
C T E R R R Q T I V P V C S Y E E R E R 240
P N C L S L Q D S C K T N Y I C R S R L 260
A D F F T N C Q P E S R S V S N C L K E 280
N Y A D C L L A Y S G L I G T V M T P N 300
Y V D S S S L S V A P W C D C S N S G N 320
D L E D C L K F L N F F K D N T C L K N 340
A I Q A F G N G S D V T M W Q P A P P V 360
Q T T T A T T T T A F R V K N K P L G P 380
A G S E N E I P T H V L P P C A N L Q A 400
Q K L K S N V S G S T H L C L S D S D F 420
G K D G L A G A S S H I T T K S M A A P 440
P S C S L S S L P V L M L T A L A A L L 460
S V S L A E T S *     468
```

Figure 5

Human GDNF receptor Clones -- Alignment to generate consensus sequence

	-237				-188
Gdnfr	AATCTGGCCT	CGGAACACGC	CATTCTCCGC	GCCGCTTCCA	ATAACCACTA
Hsgr-21af	TCTGGCCT	CGGAACACGC	CATTCTCCGC	GCCGCTTCCA	ATAACCACTA
Hsgr-21bf	AATCTGGCCT	CGGAACACGC	CATTCTCCGC	GCCGCTTCCA	ATAACCACTA
21acon	TCTGGCCT	CGGAACACGC	CATTCTCCGC	GCCGCTTCCA	ATAACCACTA
21bcon	AATCTGGCCT	CGGAACACGC	CATTCTCCGC	GCCGCTTCCA	ATAACCACTA

	-187				-138
Gdnfr	ACATCCCTAA	CGAGCATCCG	AGCCGAGGGC	TCTGCTCGGA	AATCGTCCTG
Hsgr-21af	ACATCCCTAA	CGAGCATCCG	AGCCGAGGGC	TCTGCTCGGA	AATCGTCCTG
Hsgr-21bf	ACATCCCTAA	CGAGCATCCG	AGCCGAGGGC	TCTGCTCGGA	AATCGTCCTG
21acon	ACATCCCTAA	CGAGCATCCG	AGCCGAGGGC	TCTGCTCGGA	AATCGTCCTG
21bcon	ACATCCCTAA	CGAGCATCCG	AGCCGAGGGC	TCTGCTCGGA	AATCGTCCTG

	-137				-88
Gdnfr	GCCCAACTCG	GCCCTTCGAG	CTCTCGAAGA	TTACCGCATC	TATTTTTTTT
Hsgr-21af	GCCCAACTCG	GCCCTTCGAG	CTCTCGAAGA	TTACCGCATC	TATTTTTTTT
Hsgr-21bf	GCCCAACTCG	GCCCTTCGAG	CTCTCGAAGA	TTACCGCATC	TATTTTTTTT
21acon	GCCCAACTCG	GCCCTTCGAG	CTCTCGAAGA	TTACCGCATC	TATTTTTTTT
21bcon	GCCCAACTCG	GCCCTTCGAG	CTCTCGAAGA	TTACCGCATC	TATTTTTTTT

	-87				-38
Gdnfr	TTCTTTTTTT	TCTTTTCCTA	GCGCAGATAA	AGTGAGCCCG	GAAAGGGAAG
Hsgr-21af	TTCTTTTTTT	TCTTTTCCTA	GCGCAGATAA	AGTGAGCCCG	GAAAGGGAAG
Hsgr-21bf	TTCTTTTTTT	TCTTTTCCTA	GCGCAGATAA	AGTGAGCCCG	GAAAGGGAAG
21acon	TTCTTTTTTT	TCTTTTCCTA	GCGCAGATAA	AGTGAGCCCG	GAAAGGGAAG
21bcon	TTCTTTTTTT	TCTTTTCCTA	GCGCAGATAA	AGTGAGCCCG	GAAAGGGAAG

Figure 5 (continued)

```
              -37                                                     12
     Gdnfr    GAGGGGGCGG GGACACCATT GCCCTGAAAG AATAAATAAG TAAATAAACA
 Hsgr-21af    GAGGGGGCGG GGACACCATT GCCCTGAAAG AATAAATAAG TAAATAAACA
 Hsgr-21bf    GAGGGGGCGG GGACACCATT GCCCTGAAAG AATAAATAAG TAAATAAACA
    21acon    GAGGGGGCGG GGACACCATT GCCCTGAAAG AATAAATAAG TAAATAAACA
    21bcon    GAGGGGGCGG GGACACCATT GCCCTGAAAG AATAAATAAG TAAATAAACA

              13                                                      62
     Gdnfr    AACTGGCTCC TCGCCGCAGC TGGACGCGGT CGGTTGAGTC CAGGTTGGGT
 Hsgr-21af    AACTGGCTCC TCGCCGCAGC TGGACGCGGT CGGTTGAGTC CAGGTTGGGT
 Hsgr-21bf    AACTGGCTCC TCGCCGCAGC TGGACGCGGT CGGTTGAGTC CAGGTTGGGT
    21acon    AACTGGCTCC TCGCCGCAGC TGGACGCGGT CGGTTGAGTC CAGGTTGGGT
    21bcon    AACTGGCTCC TCGCCGCAGC TGGACGCGGT CGGTTGAGTC CAGGTTGGGT

              63                                                     112
     Gdnfr    CGGACCTGAA CCCCTAAAAG CGGAACCGCC TCCCGCCCTC GCCATCCCGG
 Hsgr-21af    CGGACCTGAA CCCCTAAAAG CGGAACCGCC TCCCGCCCTC GCCATCCCGG
 Hsgr-21bf    CGGACCTGAA CCCCTAAAAG CGGAACCGCC TCCCGCCCTC GCCATCCCGG
    21acon    CGGACCTGAA CCCCTAAAAG CGGAACCGCC TCCCGCCCTC GCCATCCCGG
    21bcon    CGGACCTGAA CCCCTAAAAG CGGAACCGCC TCCCGCCCTC GCCATCCCGG

              113                                                    162
     Gdnfr    AGCTGAGTCG CCGGCGGCGG TGGCTGCTGC CAGACCCGGA GTTTCCTCTT
 Hsgr-21af    AGCTGAGTCG CCGGCGGCGG TGGCTGCTGC CAGACCCGGA GTTTCCTCTT
 Hsgr-21bf    AGCTGAGTCG CCGGCGGCGG TGGCTGCTGC CAGACCCGGA GTTTCCTCTT
    21acon    AGCTGAGTCG CCGGCGGCGG TGGCTGCTGC CAGACCCGGA GTTTCCTCTT
    21bcon    AGCTGAGTCG CCGGCGGCGG TGGCTGCTGC CAGACCCGGA GTTTCCTCTT

              163                                                    212
     Gdnfr    TCACTGGATG GAGCTGAACT TTGGGCGGCC AGAGCAGCAC AGCTGTCCGG
 Hsgr-21af    TCACTGGATG GAGCTGAACT TTGGGCGGCC AGAGCAGCAC AGCTGTCCGG
 Hsgr-21bf    TCACTGGATG GAGCTGAACT TTGGGCGGCC AGAGCAGCAC AGCTGTCCGG
    21acon    TCACTGGATG GAGCTGAACT TTGGGCGGCC AGAGCAGCAC AGCTGTCCGG
    21bcon    TCACTGGATG GAGCTGAACT TTGGGCGGCC AGAGCAGCAC AGCTGTCCGG
```

Figure 5 (continued)

```
           213                                                262
Gdnfr      GGATCGCTGC ACGCTGAGCT CCCTCGGCAA GACCCAGCGG CGGCTCGGGA
Hsgr-21af  GGATCGCTGC ACGCTGAGCT CCCTCGGCAA GACCCAGCGG CGGCTCGGGA
Hsgr-21bf  GGATCGCTGC ACGCTGAGCT CCCTCGGCAA GACCCAGCGG CGGCTCGGGA
21acon     GGATCGCTGC ACGCTGAGCT CCCTCGGCAA GACCCAGCGG CGGCTCGGGA
21bcon     GGATCGCTGC ACGCTGAGCT CCCTCGGCAA GACCCAGCGG CGGCTCGGGA

           263                                                312
Gdnfr      TTTTTTTGGG GGGGCGGGGA CCAGCCCCGC GCCGGCACCA TGTTCCTGGC
Hsgr-21af  TTTTTTTGGG
Hsgr-21bf  TTTTTTTGGG
21acon     TTTTTTTGGG GGGGCGGGGA CCAGCCCCGC GCCGGCACCA TGTTCCTGGC
21bcon     TTTTTTTGGG GGGGCGGGGA CCAGCCCCGC GCCGGCACCA TGTTCCTGGC

           313                                                362
Gdnfr      GaCCCTGTAC TTCGCGCTGC CGCTCTTGGA CTTGCTCCTG TCGGCCGAAG
21acon     GNCCCTGTAC TTCGCGCTGC CGCTCTTGGA CTTGCTCCTG TCGGCCGAAG
21bcon     GACCCTGTAC TTCGCGCTGC CGCTCTTGGA CTTGCTCCTG TCGGCCGAAG

           363                                                412
Gdnfr      TGAGCGGCGG AGACCGCCTG GATTGCGTGA AAGCCAGTGA TCAGTGCCTG
21acon     TGAGCGGCGG AGACCGCCTG GATTGCGTGA AAGCCAGTGA TCAGTGCCTG
21bcon     TGAGCGGCGG AGACCGCCTG GATTGCGTGA AAGCCAGTGA TCAGTGCCTG

           413                                                462
Gdnfr      AAGGAGCAGA GCTGCAGCAC CAAGTACCGC ACGCTAAGGC AGTGCGTGGC
21acon     AAGGAGCAGA GCTGCAGCAC CAAGTACCGC ACGCTAAGGC AGTGCGTGGC
21bcon     AAGGAGCAGA GCTGCAGCAC CAAGTACCGC ACGCTAAGGC AGTGCGTGGC

           463                                                512
Gdnfr      GGGCAAGGAG ACCAACTTCA GCCTGGCATC CGGCCTGGAG GCCAAGGATG
21acon     GGGCAAGGAG ACCAACTTCA GCCTGGCATC CGGCCTGGAG GCCAAGGATG
21bcon     GGGCAAGGAG ACCAACTTCA GCCTGGCATC CGGCCTGGAG GCCAAGGATG
```

Figure 5 (continued)

```
           513                                                562
Gdnfr      AGTGCCGCAG CGCCATGGAG GCCCTGAAGC AGAAGTCGCT CTACAACTGC
21acon     AGTGCCGCAG CGCCATGGAG GCCCTGAAGC AGAAGTCGCT CTACAACTGC
21bcon     AGTGCCGCAG CGCCATGGAG GCCCTGAAGC AGAAGTCGCT CTACAACTGC

           563                                                612
Gdnfr      CGCTGCAAGC GGGGTATGAA GAAGGAGAAG AACTGCCTGC GCATTTACTG
21acon     CGCTGCAAGC GGGGTATGAA GAAGGAGAAG AACTGCCTGC GCATTTACTG
21bcon     CGCTGCAAGC GGGGTATGAA GAAGGAGAAG AACTGCCTGC GCATTTACTG

           613                                                662
Gdnfr      GAGCATGTAC CAGAGCCTGC AGGGAAATGA TCTGCTGGAG GATTCCCCAT
21acon     GAGCATGTAC CAGAGCCTGC AGGGAAATGA TCTGCTGGAG GATTCCCCAT
21bcon     GAGCATGTAC CAGAGCCTGC AGGGAAATGA TCTGCTGGAG GATTCCCCAT

           663                                                712
Gdnfr      ATGAACCAGT TAACAGCAGA TTGTCAGATA TATTCCGGGT GGTCCCATTC
21acon     ATGAACCAGT TAACAGCAGA TTGTCAGATA TATTCCGGGT GGTCCCATTC
21bcon     ATGAACCAGT TAACAGCAGA TTGTCAGATA TATTCCGGGT GGTCCCATTC

           713                                                762
Gdnfr      ATATCAGATG TTTTTCAGCA AGTGGAGCAC ATTCCCAAAG GGAACAACTG
21acon     ATATCAGATG TTTTTCAGCA AGTGGAGCAC ATTCCCAAAG GGAACAACTG
21bcon     ATATCAGATG TTTTTCAGCA AGTGGAGCAC ATTCCCAAAG GGAACAACTG

           763                                                812
Gdnfr      CCTGGATGCA GCGAAGGCCT GCAACCTCGA CGACATTTGC AAGAAGTACA
21acon     CCTGGATGCA GCGAAGGCCT GCAACCTCGA CGACATTTGC AAGAAGTACA
21bcon     CCTGGATGCA GCGAAGGCCT GCAACCTCGA CGACATTTGC AAGAAGTACA

           813                                                862
Gdnfr      GGTCGGCGTA CATCACCCCG TGCACCACCA GCGTGTCCAA .GATGTCTGC
Hsgr-29a    GTCGGCGTA CATCACCCCG TGCACCACCA GCGTGTCCAA TGATGTCTGC
21acon     GGTCGGCGTA CATCACCCCG TGCACCACCA GCGTGTCCAA CGATGTCTGC
21bcon     GGTCGGCGTA CATCACCCCG TGCACCACCA GCGTGTCCAA CGATGTCTGC
29brc       GTCGGCGTA CATCACCCCG TGCACCACCA GCGTGTCCAA TGATGTCTGC
```

Figure 5 (continued)

```
           863                                                912
    Gdnfr  AACCGCCGCA AGTGCCACAA GGCCCTCCGG CAGTTCTTTG ACAAGGTCCC
Hsgr-29a   AACCGCCGCA AGTGCCACAA GGCCCTCCGG CAGTTCTTTG ACAAGGTCCC
   21acon  AACCGCCGCA AGTGCCACAA GGCCCTCCGG CAGTTCTTTG ACAAGGTCCC
   21bcon  AACCGCCGCA AGTGCCACAA GGCCCTCCGG CAGTTCTTTG ACAAGGTCCC
    29brc  AACCGCCGCA AGTGCCACAA GGCCCTCCGG CAGTTCTTTG ACAAGGTCCC

           913                                                962
    Gdnfr  GGCCAAGCAC AGCTACGGAA TGCTCTTCTG CTCCTGCCGG GACATCGCCT
Hsgr-29a   GGCCAAGCAC AGCTACGGAA TGCTCTTCTG CTCCTGCCGG GACATCGCCT
   21acon  GGCCAAGCAC AGCTACGGAA TGCTCTTCTG CTCCTGCCGG GACATCGCCT
   21bcon  GGCCAAGCAC AGCTACGGAA TGCTCTTCTG CTCCTGCCGG GACATCGCCT
    29brc  GGCCAAGCAC AGCTACGGAA TGCTCTTCTG CTCCTGCCGG GACATCGCCT

           963                                               1012
    Gdnfr  GCACAGAGCG GAGGCGACAG ACCATCGTGC CTGTGTGCTC CTATGAAGAG
Hsgr-29a   GCACAGAGCG GAGGCGACAG ACCATCGTGC CTGTGTGCTC CTATGAAGAG
   21acon  GCACAGAGCG GAGGCGACAG ACCATCGTGC CTGTGTGCTC CTATGAAGAG
   21bcon  GCACAGAGCG GAGGCGACAG ACCATCGTGC CTGTGTGCTC CTATGAAGAG
    29brc  GCACAGAGCG GAGGCGACAG ACCATCGTGC CTGTGTGCTC CTATGAAGAG

           1013                                              1062
    Gdnfr  AGGGAGAAGC CCAACTGTTT GAATTTGCAG GACTCCTGCA AGACGAATTA
Hsgr-21ar                        GAATTTGCAG GACTCCTGCA AGACGAATTA
Hsgr-21br                                                       A
Hsgr-29a   AGGGAGAAGC CCAACTGTTT GAATTTGCAG GACTCCTGCA AGACGAATTA
   21acon  AGGGAGAAGC CCAACTGTTT GAATTTGCAG GACTCCTGCA AGACGAATTA
   21bcon  AGGGAGAAGC CCAACTGTTT GAATTTGCAG GACTCCTGCA AGACGAATTA
    29brc  AGGGAGAAGC CCAACTGTTT GAATTTGCAG GACTCCTGCA AGACGAATTA
```

Figure 5 (continued)

```
          1063                                                1112
Gdnfr     CATCTGCAGA TCTCGCCTTG CGGATTTTTT TACCAACTGC CAGCCAGAGT
Hsgr-21ar CATCTGCAGA TCTCGCCTTG CGGATTTTTT TACCAACTGC CAGCCAGAGT
Hsgr-21br CATCTGCAGA TCTCGCCTTG CGGATTTTTT TACCAACTGC CAGCCAGAGT
Hsgr-29a  CATCTGCAGA TCTCGCCTTG CGGATTTTTT TACCAACTGC CAGCCAGAGT
21acon    CATCTGCAGA TCTCGCCTTG CGGATTTTTT TACCAACTGC CAGCCAGAGT
21bcon    CATCTGCAGA TCTCGCCTTG CGGATTTTTT TACCAACTGC CAGCCAGAGT
29brc     CATCTGCAGA TCTCGCCTTG CGGATTTTTT TACCAACTGC CAGCCAGAGT

          1113                                                1162
Gdnfr     CAAGGTCTGT CAGCAGCTGT CTAAAGGAAA ACTACGCTGA CTGCCTCCTC
Hsgr-21ar CAAGGTCTGT CAGCAGCTGT CTAAAGGAAA ACTACGCTGA CTGCCTCCTC
Hsgr-21br CAAGGTCTGT CAGCAGCTGT CTAAAGGAAA ACTACGCTGA CTGCCTCCTC
Hsgr-29a  CAAGGTCTGT CAGCAGCTGT CTAAAGGAAA ACTACGCTGA CTGCCTCCTC
21acon    CAAGGTCTGT CAGCAGCTGT CTAAAGGAAA ACTACGCTGA CTGCCTCCTC
21bcon    CAAGGTCTGT CAGCAGCTGT CTAAAGGAAA ACTACGCTGA CTGCCTCCTC
29brc     CAAGGTCTGT CAGCAGCTGT CTAAAGGAAA ACTACGCTGA CTGCCTCCTC

          1163                                                1212
Gdnfr     GCCTACTCGG GGCTTATTGG CACAGTCATG ACCCCCAACT ACATAGACTC
Hsgr-21ar GCCTACTCGG GGCTTATTGG CACAGTCATG ACCCCCAACT ACATAGACTC
Hsgr-21br GCCTACTCGG GGCTTATTGG CACAGTCATG ACCCCCAACT ACATAGACTC
Hsgr-29a  GCCTACTCGG GGCTTATTGG CACAGTCATG ACCCCCAACT ACATAGACTC
21acon    GCCTACTCGG GGCTTATTGG CACAGTCATG ACCCCCAACT ACATAGACTC
21bcon    GCCTACTCGG GGCTTATTGG CACAGTCATG ACCCCCAACT ACATAGACTC
29brc     GCCTACTCGG GGCTTATTGG CACAGTCATG ACCCCCAACT ACATAGACTC

          1213                                                1262
Gdnfr     CAGTAGCCTC AGTGTGGCCC CATGGTGTGA CTGCAGCAAC AGTGGGAACG
Hsgr-2                                                TGGGAACG
Hsgr-21ar CAGTAGCCTC AGTGTGGCCC CATGGTGTGA CTGCAGCAAC AGTGGGAACG
Hsgr-21br CAGTAGCCTC AGTGTGGCCC CATGGTGTGA CTGCAGCAAC AGTGGGAACG
Hsgr-29a  CAGTAGCCTC AGTGTGGCCC CATGGTGTGA CTGCAGCAAC AGTGGGAACG
21acon    CAGTAGCCTC AGTGTGGCCC CATGGTGTGA CTGCAGCAAC AGTGGGAACG
21bcon    CAGTAGCCTC AGTGTGGCCC CATGGTGTGA CTGCAGCAAC AGTGGGAACG
29brc     CAGTAGCCTC AGTGTGGCCC CATGGTGTGA CTGCAGCAAC AGTGGGAACG
```

Figure 5 (continued)

	1263				1312
Gdnfr	ACCTAGAAGA	GTGCTTGAAA	TTTTTGAATT	TCTTCAAGGA	CAATACATGT
Hsgr-2	ACCTAGAAGA	GTGCTTGAAA	TTTTTGAATT	TCTTCAAGGA	CAATACATGT
Hsgr-9	A	GTGCTTGAAA	TTTTTGAATT	TCTTCAAGGA	CAATACATGT
Hsgr-21ar	ACCTAGAAGA	GTGCTTGAAA	TTTTTGAATT	TCTTCAAGGA	CAATACATGT
Hsgr-21br	ACCTAGAAGA	GTGCTTGAAA	TTTTTGAATT	TCTTCAAGGA	CAATACATGT
Hsgr-29a	ACCTAGAAGA	GTGCTTGAAA	TTTTTGAATT	TCTTCAAGGA	CAATACATGT
21acon	ACCTAGAAGA	GTGCTTGAAA	TTTTTGAATT	TCTTCAAGGA	CAATACATGT
21bcon	ACCTAGAAGA	GTGCTTGAAA	TTTTTGAATT	TCTTCAAGGA	CAATACATGT
29brc	ACCTAGAAGA	GTGCTTGAAA	TTTTTGAATT	TCTTCAAGGA	CAATACATGT

	1313				1362
Gdnfr	CTTAAAAATG	CAATTCAAGC	CTTTGGCAAT	GGCTCCGATG	TGACCGTGTG
Hsgr-2	CTTAAAAATG	CAATTCAAGC	CTTTGGCAAT	GGCTCCGATG	TGACCGTGTG
Hsgr-9	CTTAAAAATG	CAATTCAAGC	CTTTGGCAAT	GGCTCCGATG	TGACCGTGTG
Hsgr-21ar	CTTAAAAATG	CAATTCAAGC	CTTTGGCAAT	GGCTCCGATG	TGACCGTGTG
Hsgr-21br	CTTAAAAATG	CAATTCAAGC	CTTTGGCAAT	GGCTCCGATG	TGACCGTGTG
Hsgr-29a	CTTAAAAATG	CAATTCAAGC	CTTTGGCAAT	GGCTCCGATG	TGACCGTGTG
21acon	CTTAAAAATG	CAATTCAAGC	CTTTGGCAAT	GGCTCCGATG	TGACCGTGTG
21bcon	CTTAAAAATG	CAATTCAAGC	CTTTGGCAAT	GGCTCCGATG	TGACCGTGTG
29brc	CTTAAAAATG	CAATTCAAGC	CTTTGGCAAT	GGCTCCGATG	TGACCGTGTG

	1363				1412
Gdnfr	GCAGCCAGCC	TTCCCAGTAC	AGACCACCAC	TGCCaCTACC	ACCACTGCCC
Hsgr-2	GCAGCCAGCC	TTCCCAGTAC	AGACCACCAC	TGCCACTACC	ACCACTGCCC
Hsgr-9	GCAGCCAGCC	TTCCCAGTAC	AGACCACCAC	TGCCACTACC	ACCACTGCCC
Hsgr-21ar	GCAGCCAGCC	TTCCCAGTAC	AGACCACCAC	TGCCACTACC	ACCACTGCCC
Hsgr-21br	GCAGCCAGCC	TTCCCAGTAC	AGACCACCAC	TGCCACTACC	ACCACTGCCC
Hsgr-29a	GCAGCCAGCC	TTCCCAGTAC	AGACCACCAC	TGCCGCTACC	ACCACTGCCC
21acon	GCAGCCAGCC	TTCCCAGTAC	AGACCACCAC	TGCCACTACC	ACCACTGCCC
21bcon	GCAGCCAGCC	TTCCCAGTAC	AGACCACCAC	TGCCACTACC	ACCACTGCCC
29brc	GCAGCCAGCC	TTCCCAGTAC	AGACCACCAC	TGCCGCTACC	ACCACTGCCC

Figure 5 (continued)

```
          1413                                                   1462
Gdnfr     TCCGGGTTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT
Hsgr-2    TCCGGGTTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT
Hsgr-9    TCCGGGTTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT
Hsgr-21ar TCCGGGTTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT
Hsgr-21br TCCGGGTTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT
Hsgr-29a  TCCGGGTTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT
21acon    TCCGGGTTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT
21bcon    TCCGGGTTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT
29brc     TCCGGGTTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT

          1463                                                   1512
Gdnfr     CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA
Hsgr-2    CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA
Hsgr-9    CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA
Hsgr-21ar CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA
Hsgr-21br CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA
Hsgr-29a  CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA
21acon    CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA
21bcon    CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA
29brc     CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA

          1513                                                   1562
Gdnfr     ATCCAATGTG TCGGGCAATA CACACCTCTG TATTTCCAAT GGTAATTATG
Hsgr-2    ATCCAATGTG TCGGGCAATA CACACCTCTG TATTTCCAAT GGTAATTATG
Hsgr-9    ATCCAATGTG TCGGGCAATA CACACCTCTG TATTTCCAAT GGTAATTATG
Hsgr-21ar ATCCAATGTG TCGGGCAATA CACACCTCTG TATTTCCAAT GGTAATTATG
Hsgr-21br ATCCAATGTG TCGGGCAATA CACACCTCTG TATTTCCAAT GGTAATTATG
21acon    ATCCAATGTG TCGGGCAATA CACACCTCTG TATTTCCAAT GGTAATTATG
21bcon    ATCCAATGTG TCGGGCAATA CACACCTCTG TATTTCCAAT GGTAATTATG
29brc     ATCCAATGTG TCGGGCAATA CACACCTCTG TATTTCCAAT GGTAATTATG
```

Figure 5 (continued)

	1563				1612
Gdnfr	AAAAAGAAGG	TCTCGGTGCT	TCCAGCCACA	TAACCACAAA	ATCAATGGCT
Hsgr-2	AAAAAGAAGG	TCTCGGTGCT	TCCAGCCACA	TAACCACAAA	ATCAATGGCT
Hsgr-9	AAAAAGAAGG	TCTCGGTGCT	TCCAGCCACA	TAACCACAAA	ATCAATGGCT
Hsgr-21ar	AAAAAGAAGG	TCTCGGTGCT	TCCAGCCACA	TAACCACAAA	ATCAATGGCT
Hsgr-21br	AAAAAGAAGG	TCTCGGTGCT	TCCAGCCACA	TAACCACAAA	ATCAATGGCT
21acon	AAAAAGAAGG	TCTCGGTGCT	TCCAGCCACA	TAACCACAAA	ATCAATGGCT
21bcon	AAAAAGAAGG	TCTCGGTGCT	TCCAGCCACA	TAACCACAAA	ATCAATGGCT
29brc	AAAAAGAAGG	TCTCGGTGCT	TCCAGCCACA	TAACCACAAA	ATCAATGGCT

	1613				1662
Gdnfr	GCTCCTCCAA	GCTGTGGTCT	GAGCCCACTG	CTGGTCCTGG	TGGTAACCGC
Hsgr-2	GCTCCTCCAA	GCTGTGGTCT	GAGCCCACTG	CTGGTCCTGG	TGGTAACCGC
Hsgr-9	GCTCCTCCAA	GCTGTGGTCT	GAGCCCACTG	CTGGTCCTGG	TGGTAACCGC
Hsgr-21ar	GCTCCTCCAA	GCTGTGGTCT	GAGCCCACTG	CTGGTCCTGG	TGGTAACCGC
Hsgr-21br	GCTCCTCCAA	GCTGTGGTCT	GAGCCCACTG	CTGGTCCTGG	TGGTAACCGC
21acon	GCTCCTCCAA	GCTGTGGTCT	GAGCCCACTG	CTGGTCCTGG	TGGTAACCGC
21bcon	GCTCCTCCAA	GCTGTGGTCT	GAGCCCACTG	CTGGTCCTGG	TGGTAACCGC
29brc	GCTCCTCCAA	GCTGTGGTCT	GAGCCCACTG	CTGGTCCTGG	TGGTAACCGC

	1663				1712
Gdnfr	TCTGTCCACC	CTATTATCTT	TAACAGAAAC	ATCATAGCTG	CATTAAAAAA
Hsgr-2	TCTGTCCACC	CTATTATCTT	TAACAGAAAC	ATCATAGCTG	CATTAAAAAA
Hsgr-9	TCTGTCCACC	CTATTATCTT	TAACAGAAAC	ATCATAGCTG	CATTAAAAAA
Hsgr-21ar	TCTGTCCACC	CTATTATCTT	TAACAGAAA		
Hsgr-21br	TCTGTCCACC	CTATTATCTT	TAACAGAAA		
21acon	TCTGTCCACC	CTATTATCTT	TAACAGAAA		
21bcon	TCTGTCCACC	CTATTATCTT	TAACAGAAA		
29brc	TCTGTCCACC	CTATTATCTT	TAACAGAAAC	ATCATAGCTG	CATTAAAAAA

	1713				1762
Gdnfr	ATACAATATG	GACATGTAAA	AAGACAAAAA	CCAAGTTATC	TGTTTCCTGT
Hsgr-2	ATACAATATG	GACATGTAAA	AAGACAAAAA	CCAAGTTATC	TGTTTCCTGT
Hsgr-9	ATACAATATG	GACATGTAAA	AAGACAAAAA	CCAAGTTATC	TGTTTCCTGT
29brc	ATACAATATG	GACATGTAAA	AAGACAAAAA	CCAAGTTATC	TGTTTCCTGT

Figure 5 (continued)

```
         1763                                                   1812
Gdnfr    TCTCTTGTAT AGCTGAAATT CCAGTTTAGG AGCTCAGTTG AGAAACAGTT
Hsgr-2   TCTCTTGTAT AGCTGAAATT CCAGTTTAGG AGCTCAGTTG AGAAACAGTT
Hsgr-9   TCTCTTGTAT AGCTGAAATT CCAGTTTAGG AGCTCAGTTG AGAAACAGTT
29brc    TCTCTTGTAT AGCTGAAATT CCAGTTTAGG AGCTCAGTTG AGAAACAGTT

         1813                                                   1862
Gdnfr    CCATTCAACT GGAACATTTT TTTTTTT.CC TTTTAAGAAA GCTTCTTGTG
Hsgr-2   CCATTCAACT GGAACATTTT TTTTTTT.CC TTTTAAGAAA GCTTCTTGTG
Hsgr-9   CCATTCAACT GGAACATTTT TTTTTTTTCC TTTTAAGAAA GCTTCTTGTG
29brc    CCATTCAACT GGAACATTTT TTTTTTT.CC TTTTAAGAAA GCTTCTTGTG

         1863                                                   1912
Gdnfr    ATCCTTcGGG GCTTCTGTGA AAAACCTGAT GCAGTGCTCC ATCCAAACTC
Hsgr-2   ATCCTTCGGG GCTTCTGTGA AAAACCTGAT GCAGTGCTCC ATCCAAACTC
Hsgr-9   ATCCTTTGGG GCTTCTGTGA AAAACCTGAT GCAGTGCTCC ATCCAAACTC
29brc    ATCCTTCGGG GCTTCTGTGA AAAACCTGAT GCAGTGCTCC ATCCAAACTC

         1913                                                   1962
Gdnfr    AGAAGGCTTT GGGATATGCT GTATTTTAAA GGGACAGTTT GTAACTTGGG
Hsgr-2   AGAAGGCTTT GGGATATGCT GTATTTTAAA GGGACAGTTT GTAACTTGGG
Hsgr-9   AGAAGGCTTT GGGATATGCT GTATTTTAAA GGGACAGTTT GTAACTTGGG
29brc    AGAAGGCTTT GGGATATGCT GTATTTTAAA GGGACAGTTT GTAACTTGGG

         1963                                                   2012
Gdnfr    CTGTAAAGCA AACTGGGGCT GTGTTTTCGA TGATGATGAT cATCATGATc
Hsgr-2   CTGTAAAGCA AACTGGGGCT GTGTTTTCGA TGATGATGAT CATCATGATC
Hsgr-9   CTGTAAAGCA AACTGGGGCT GTGTTTTCGA TGATGATGAT GATCATGATG
29brc    CTGTAAAGCA AACTGGGGCT GTGTTTTCGA TGATGATGAT CATCATGATC

         2013                                                   2062
Gdnfr    ATGAT..... .......... .......... .......... ....GATTTT
Hsgr-2   ATGAT..... .......... .......... .......... ....GATTTT
Hsgr-9   ATGATCATCA TGATCATGAT GATGATCATC ATGATCATGA TGATGATTTT
29brc    ATGAT..... .......... .......... .......... ....GATTTT
```

Figure 5 (continued)

```
          2063                                                2112
Gdnfr     AACAGTTTTA CTTCTGGCCT TTCCTAGCTA GAGAAGGAGT TAATATTTCT
Hsgr-2    AACAGTTTTA CTTCTGGCCT TTCCTAGCTA GAGAAGGAGT TAATATTTCT
Hsgr-9    AACAGTTTTA CTTCTGGCCT TTCCTAGCTA GAGAAGGAGT TAATATTTCT
29brc     AACAGTTTTA CTTCTGGCCT TTCCTAGCTA GAGAAGGAGT TAATATTTCT

          2113                                                2162
Gdnfr     AAGGTAACTC CCATATCTCC TTTAATGACA TTGATTTCTA ATGATATAAA
Hsgr-2    AAGGTAACTC CCATATCTCC TTTAATGACA TTGATTTCTA ATGATATAAA
Hsgr-9    AAGGTAACTC CCATATCTCC TTTAATGACA TTGATTTCTA ATGATATAAA
29brc     AAGGTAACTC CCATATCTCC TTTAATGACA TTGATTTCTA ATGATATAAA

          2163                                                2212
Gdnfr     TTTCAGCCTA CATTGATGCC AAGCTTTTTT GCCACAAAGA AGATTCTTAC
Hsgr-2    TTTCAGCCTA CATTGATGCC AAGCTTTTTT GCCACAAAGA AGATTCTTAC
Hsgr-9    TTTCAGCCTA CATTGATGCC AAGCTTTTTT GCCACAAAGA AGATTCTTAC
29brc     TTTCAGCCTA CATTGATGCC AAGCTTTTTT GCCACAAAGA AGATTCTTAC

          2213                                                2262
Gdnfr     CAAGAGTGGG CTTTGTGGAA ACAGCTGGTA CTGATGTTCA CCTTTATATA
Hsgr-2    CAAGAGTGGG CTTTGTGGAA ACAGCTGGTA CTGATGTTCA CCTTTATATA
Hsgr-9    CAAGAGTGGG CTTTGTGGAA ACAGCTGGTA CTGATGTTCA CCTTTATATA
29brc     CAAGAGTGGG CTTTGTGGAA ACAGCTGGTA CTGATGTTCA CCTTTATATA

          2263                                                2312
Gdnfr     TGTACTAGCA TTTTCCACGC TGATGTTTAT GTACTGTAAA CAGTTCTGCA
Hsgr-2    TGTACTAGCA TTTTCCACGC TGATGTTTAT GTACTGTAAA CAGTTCTGCA
Hsgr-9    TGTACTAGCA TTTTCCACGC TGATGTTTAT GTACTGTAAA CAGTTCTGCA
29brc     TGTACTAGCA TTTTCCACGC TGATGTTTAT GTACTGTAAA CAGTTCTGCA

          2313                                                2362
Gdnfr     CTCTTGTACA AAAGAAAAAA CACCTGTCAC ATCCAAATAT AGTATCTGTC
Hsgr-2    CTCTTGTACA AAAGAAAA
Hsgr-9    CTCTTGTACA AAAGAAAA
29brc     CTCTTGTACA AAAGAAAAAA CACCTGTCAC ATCCAAATAT AGTATCTGTC
```

Figure 5 (continued)

```
       2363                                                 2412
Gdnfr  TTTTCGTCAA AATAGAGAGT GGGGAATGAG TGTGCCGATT CAATACCTCA
29brc  TTTTCGTCAA AATAGAGAGT GGGGAATGAG TGTGCCGATT CAATACCTCA

       2413                                                 2462
Gdnfr  ATCCCTGAAC GACACTCTCC TAATCCTAAG CCTTACCTGA GTGAGAAGCC
29brc  ATCCCTGAAC GACACTCTCC TAATCCTAAG CCTTACCTGA GTGAGAAGCC

       2463                                                 2512
Gdnfr  CTTTACCTAA CAAAAGTCCA ATATAGCTGA AATGTCGCTC TAATACTCTT
29brc  CTTTACCTAA CAAAAGTCCA ATATAGCTGA AATGTCGCTC TAATACTCTT

       2513                                                 2562
Gdnfr  TACACATATG AGGTTATATG TAGAAAAAAA TTTTACTACT AAATGATTTC
29brc  TACACATATG AGGTTATATG TAGAAAAAAA TTTTACTACT AAATGATTTC

       2563                                                 2612
Gdnfr  AACTATTGGC TTTCTATATT TTGAAAGTAA TGATATTGTC TCATTTTTTT
29brc  AACTATTGGC TTTCTATATT TTGAAAGTAA TGATATTGTC TCATTTTTTT

       2613                                                 2662
Gdnfr  ACTGATGGTT TAATACAAAA TACACAGAGC TTGTTTCCCC TCATAAGTAG
29brc  ACTGATGGTT TAATACAAAA TACACAGAGC TTGTTTCCCC TCATAAGTAG

       2663                                                 2712
Gdnfr  TGTTCGCTCT GATATGAACT TCACAAATAC AGCTCATCAA AAGCAGACTC
29brc  TGTTCGCTCT GATATGAACT TCACAAATAC AGCTCATCAA AAGCAGACTC

       2713                                                 2762
Gdnfr  TGAGAAGCCT CGTGCTGTAG CAGAAAGTTC TGCATCATGT GACTGTGGAC
29brc  TGAGAAGCCT CGTGCTGTAG CAGAAAGTTC TGCATCATGT GACTGTGGAC

       2763                                                 2812
Gdnfr  AGGCAGGAGG AAACAGAACA GACAAGCATT GTCTTTTGTC ATTGCTCGAA
29brc  AGGCAGGAGG AAACAGAACA GACAAGCATT GTCTTTTGTC ATTGCTCGAA
```

Figure 5 (continued)

	2813				2862
Gdnfr	GTGCAAGCGT	GCATACCTGT	GGAGGGAACT	GGTGGCTGCT	TGTAAATGTT
29brc	GTGCAAGCGT	GCATACCTGT	GGAGGGAACT	GGTGGCTGCT	TGTAAATGTT

	2863				2912
Gdnfr	CTGCAGCATC	TCTTGACACA	CTTGTCATGA	CACAATCCAG	TACCTTGGTT
29brc	CTGCAGCATC	TCTTGACACA	CTTGTCATGA	CACAATCCAG	TACCTTGGTT

	2913				2962
Gdnfr	TTCAGGTTAT	CTGACAAAGG	CAGCTTTGAT	TGGGACATGG	AGGCATGGGC
29brc	TTCAGGTTAT	CTGACAAAGG	CAGCTTTGAT	TGGGACATGG	AGGCATGGGC

	2963
Gdnfr	AGGCCGGAA
29brc	AGGCCGGAA

Figure 6

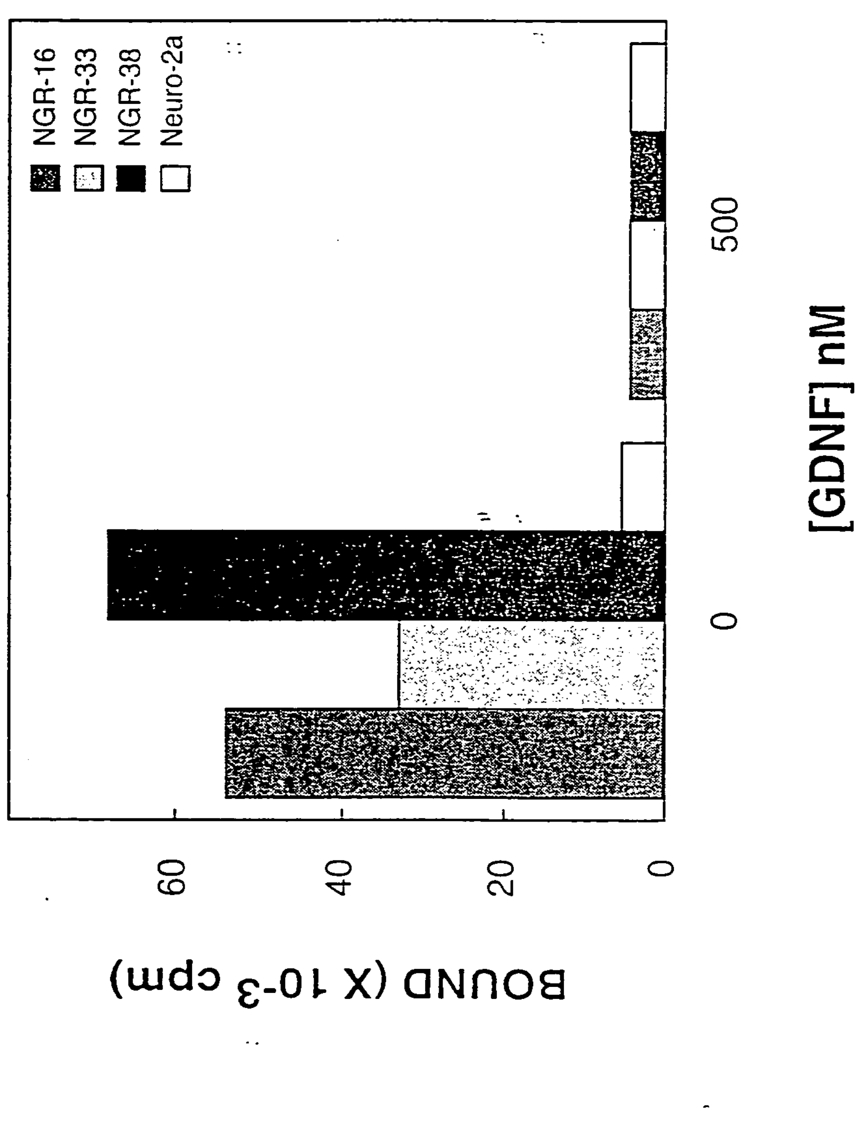

NGR-16
NGR-33
NGR-38
Neuro-2a
0
500
[GDNF] nM
0
20
40
60
BOUND (X 10-3 cpm)

Figure 7A

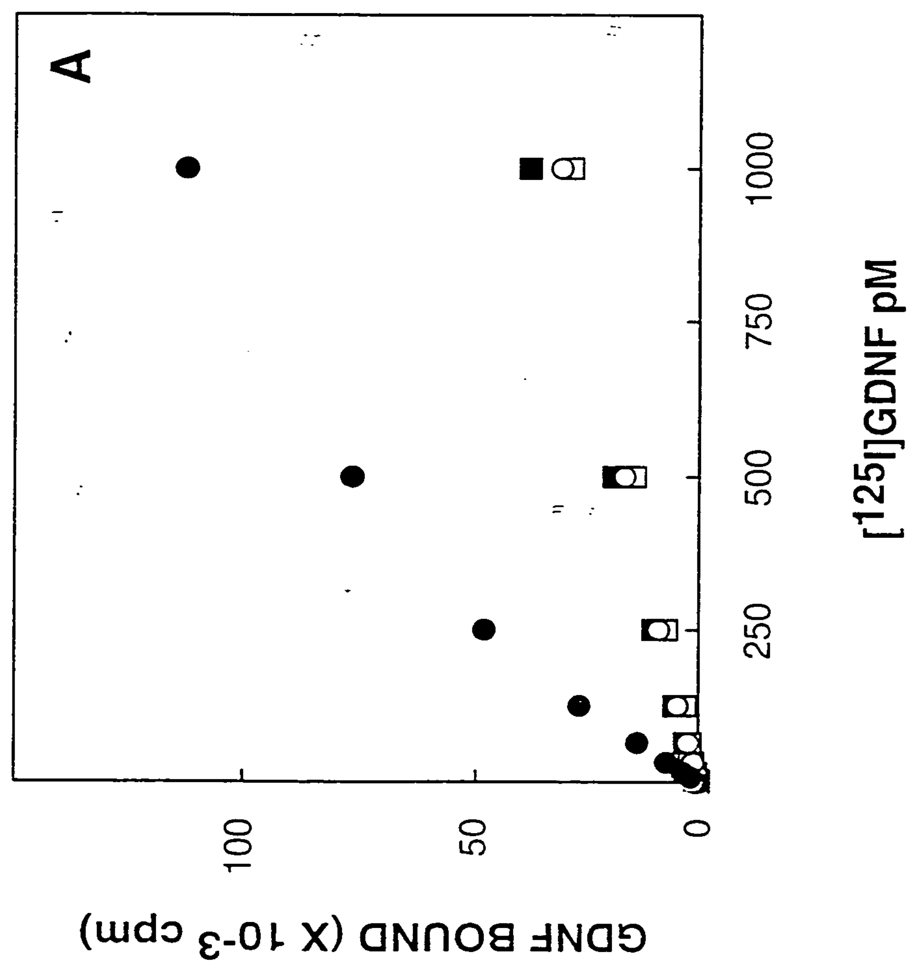


Figure 7B

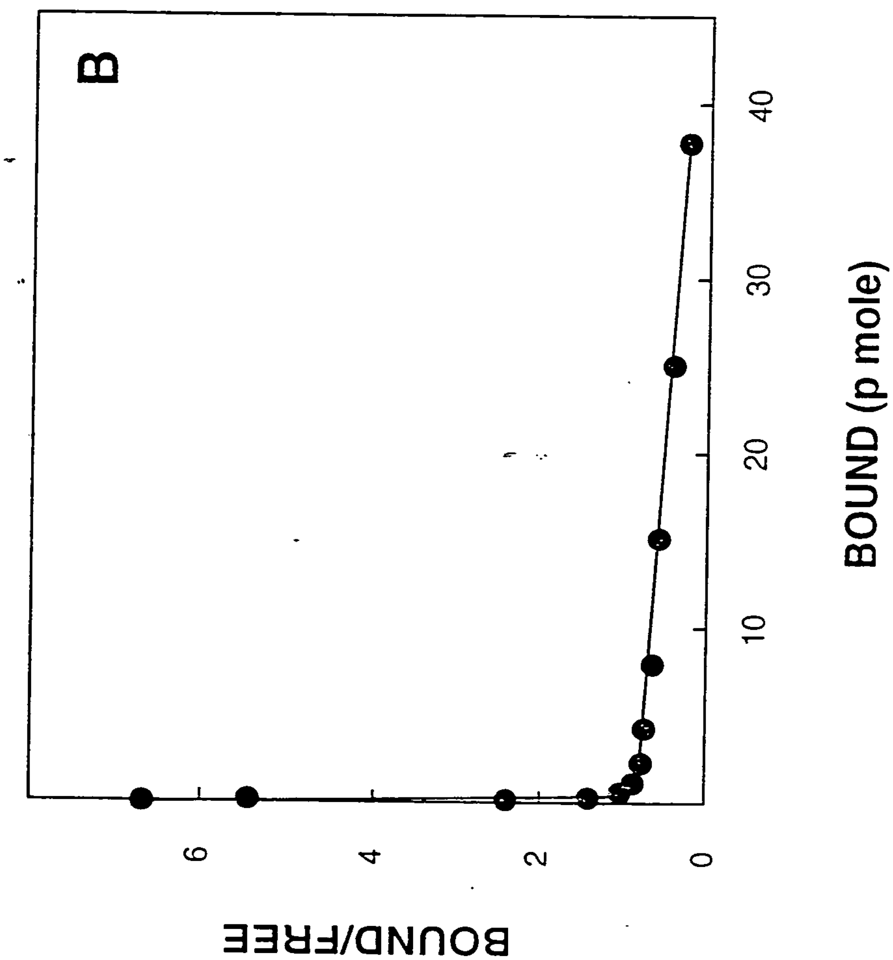


Figure 8

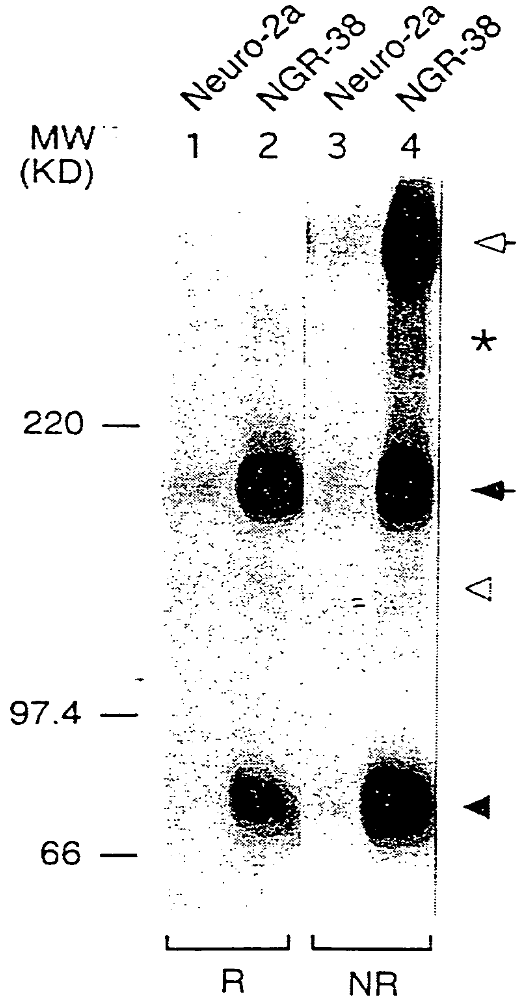
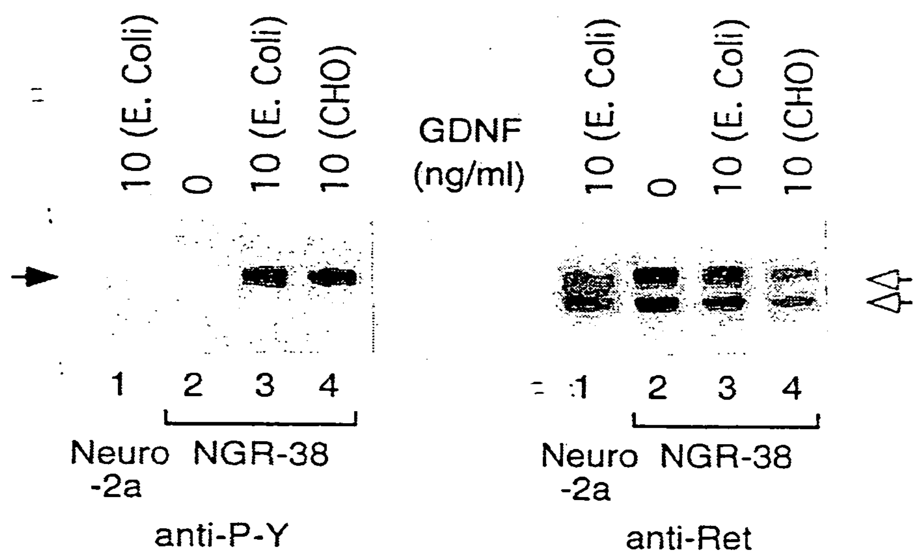


Figure 9A


GDNF
(ng/ml)
10 (E. Coli)
0
10 (E. Coli)
10 (CHO)
10 (E. Coli)
0
10 (E. Coli)
10 (CHO)
1
2
3
4
1
2
3
4
Neuro
-2a
NGR-38
Neuro
-2a
NGR-38
anti-P-Y
anti-Ret

A

Figure 9B

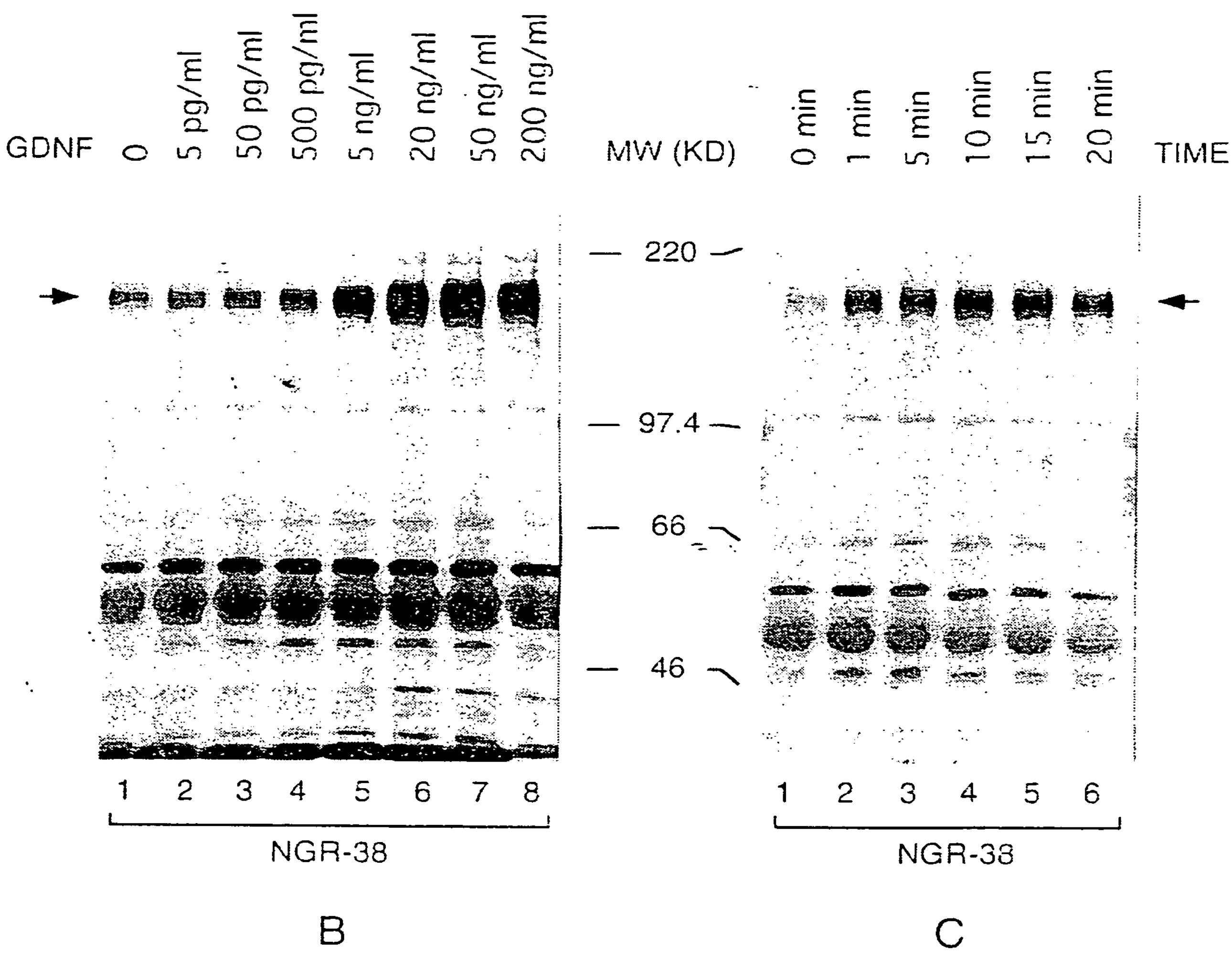
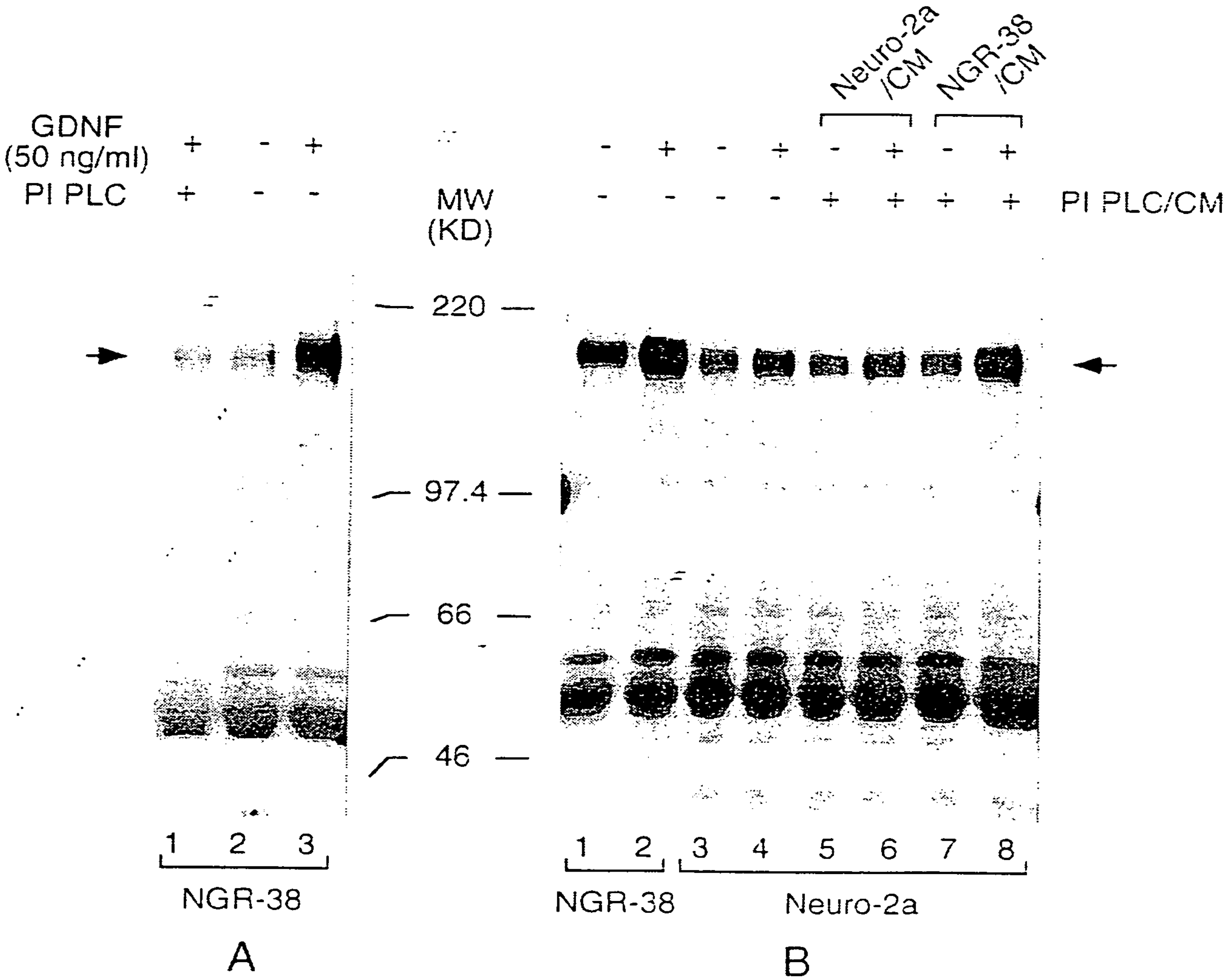
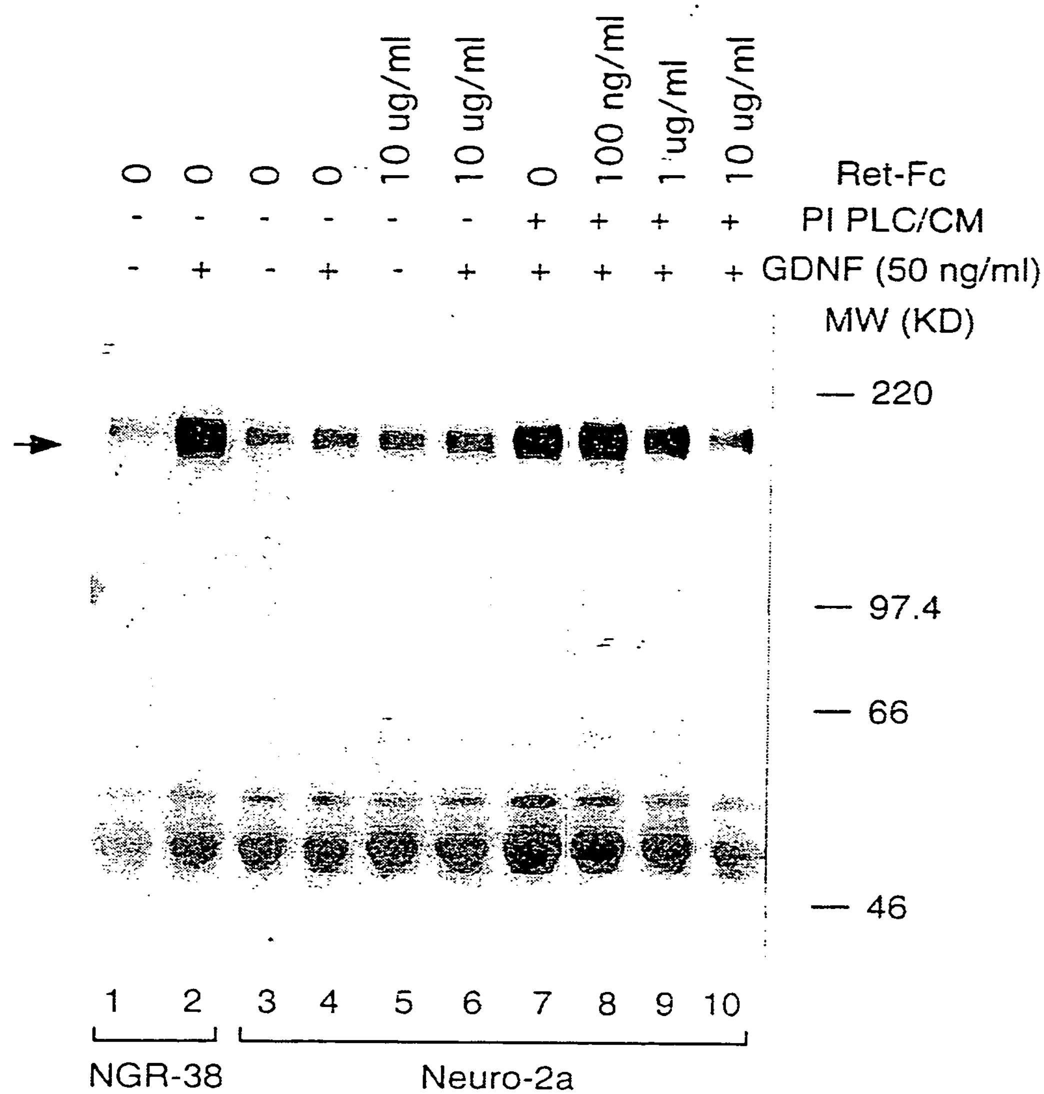

GDNF
0
5 pg/ml
50 pg/ml
500 pg/ml
5 ng/ml
20 ng/ml
50 ng/ml
200 ng/ml
MW (KD)
0 min
1 min
5 min
10 min
15 min
20 min
TIME
220
97.4
66
46
1 2 3 4 5 6 7 8
NGR-38
1 2 3 4 5 6
NGR-38
B
C

Figure 10



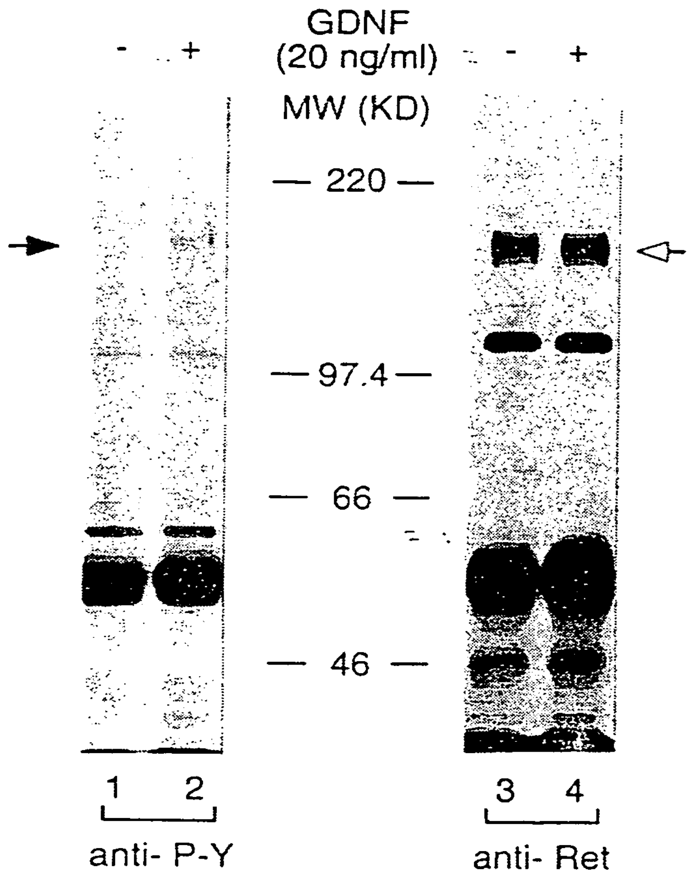
Neuro-2a /CM
NGR-38 /CM
GDNF (50 ng/ml)
PI PLC
MW (KD)
PI PLC/CM
220
97.4
66
46
1 2 3
NGR-38
1 2 3 4 5 6 7 8
NGR-38
Neuro-2a
A
B

Figure 11



Ret-Fc
0 0 0 0 10 ug/ml 10 ug/ml 0 100 ng/ml 1 ug/ml 10 ug/ml
PI PLC/CM
- - - - - - + + + +
GDNF (50 ng/ml)
- + - + - + + + + +
MW (KD)
220
97.4
66
46
1 2 3 4 5 6 7 8 9 10
NGR-38
Neuro-2a

Figure 12



GDNF Signaling Model

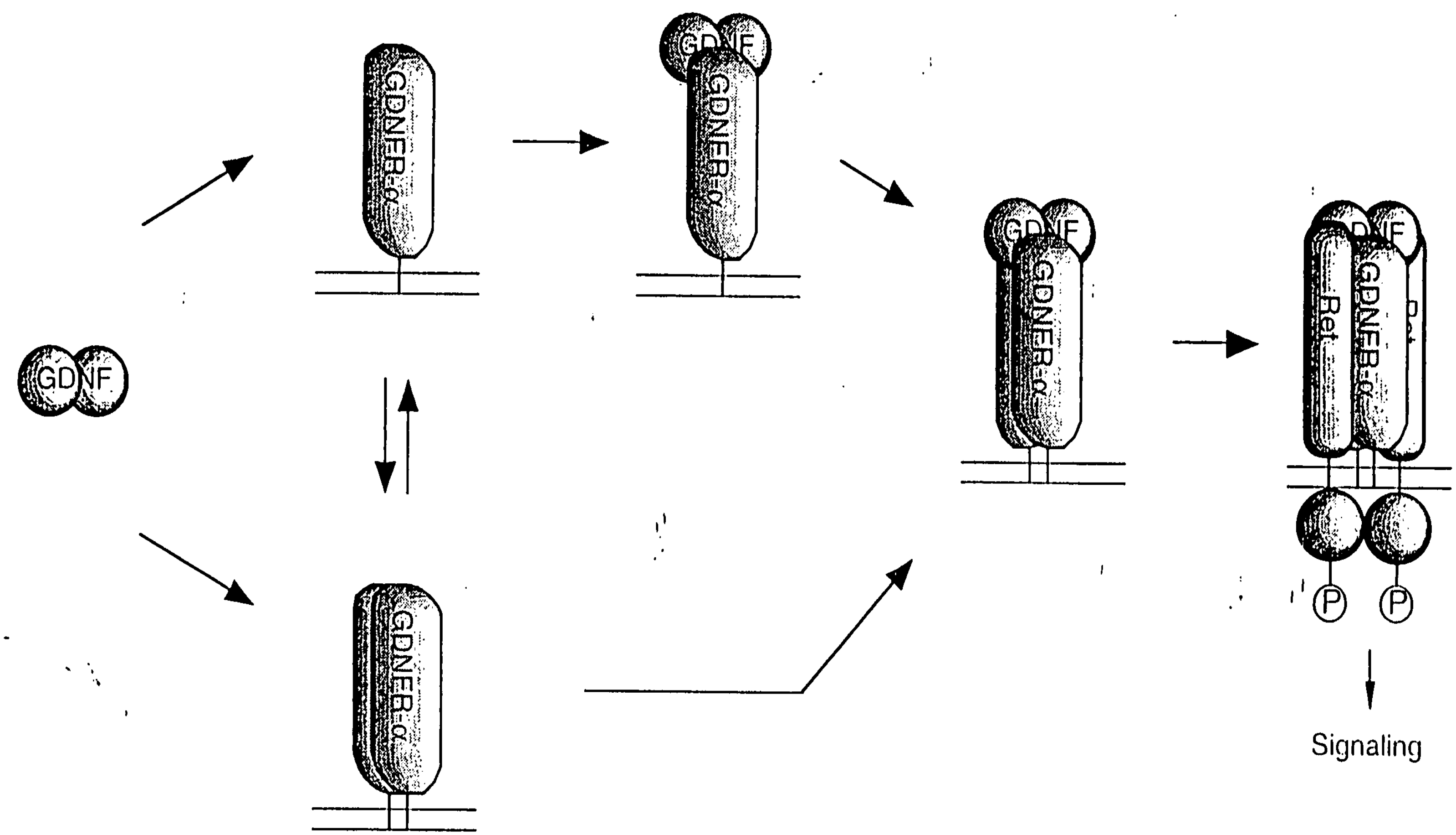


Figure 13

Figure 14

Human GRR2

```
   1  CATGAAGAAACCTCAGTAAGTCTCAGACTTGGCCCAAAGGAGCCCAACTAGTTACTCCCT    60
  61  GGTCTGTTACAGAGGATCTGGCTATTACACTCAACAGCAAAAATTCAATTCAATCCCGCT   120
 121  AAAGATATAAGAATCACTAGGAAKAATAAGCCAGAACTCAAGACAGAAATAGCATTAAGT   180
 181  AGTTCCTTCAGTACAGTGAGCAGAAGCTGGCCACTCTACGACTCTAWAAGACTCAGAAAA   240
 241  GCTTACTAGGGACCWCTGGGCATWCCGGTGTCCTATGTGGGGATTTCGTAACGTCTTTGA   300
 301  GTCAGAAGCTGCCCTCAAAATAGTTTCTTCTCAAAACGGTTTCAGGCTTTGTTAGAAAGG   360
 361  GAAGACTTCACTGCCACTTTACCCAGATCATCTACCCCATCCTTGGAATGAATGGGGAAG   420
 421  CTTCAGCCACCCTACCAGGCTCCTAAAATCACCAACTTGAGAGAAAAACTATAACGTTGC   480
 481  TCTACCAGTACTTCAGGAGGTTAAAGAAAGTCACAGAAGAAAAGAACTCTGGGGAAAACA   540
 541  GTCAAATTCGGCTATTAAGACATTAGTTACAGGCCCCTGTACCTCTCCTCTAGAAACCCT   600
 601  GGGAGTACACCCGCAGAGGAGAGAGAGCCCAAGCCACCAAGCAAAGTCAACCAATCTGGC   660
 661  AAAGGGGCGTCCCACTGCGGCTTTCAGTCCAAGAAGTGGATCCTGCTGGTTCGCAGTCTC   720
 721  TCTTCTATCTCCTCACTTCCTATTTACCCTTTGAAGTGGGTACTGAATAGCCCGTTCCCA   780
 781  AGCAGAGGCCCTTTGTATACGGGGTGCTACAGTCGCCTGGTGGAAACACCTTGGCAGAGT   840
 841  TGTTTGGTGCCAGGATGGGCCACTGAAGGCATCTGCTGTGGACACACACACACACACACA   900
 901  CACACACACACACACACACACAGAGAGAGGAGAGAGAAAGACACACGCACGCAGAGACACAC   960
 961  GGTCACTGGAATTCCATTAGAAAAAAGTGAGCCGAGCAAGGGTTAGCGGGAGAAGATTTT  1020
1021  TTTGAATCTTGTCTTCGTCTTGGTGCGAAAGAAGCGACTCCAGTCTCTCGTCCTCGAAGC  1080
1081  TCCGACTGGATTGTTCTTGGGCGCTGACACCCGTCTGTGGATTTCTTTTCTATTTGCATT  1140
```

```
1141  TTATTCCGACCCCCTCCCTCGCCGCTTCCTTCCAGCCCTTCACTCGCAAATCGCCTCTCT  1200

1201  CCCCACCTCCCCAGGCCCCTCCTGGGAAGCGCAGGGGAATTGGACCCGCGGGGACTCACG  1260

1261  CCTTCCCGGACGATTGGAGGGGAGGGCTGACCCCAGGACTGGGCTGTTGGCTTAGAAAGC  1320

1321  CGATACACAGATACGCGTATATTTGATTGTAGCGGGCAAGGGGGGCGTCGAGAGGCAGCA  1380

1381  GCCCATCGCCCGCCTCTCACCCCACCCCCTCCAGCCAGAGGCGAGAATCGCAGGACTCGG  1440

1441  GATCTTCATCGGGTGGACTAGCTGGGATCTCCGCATTGGATTTGGGGCTGATTACCACTG  1500

1501  CTTGGCTATTATTATTGTTGTTGTTACTACTATTATTTTTTTTACCCAAGGGAGAAAGA  1560

1561  CAAAAAAACGGTGGGATTTATTTAACATGATCTTGGCAAACGTCTTCTGCCTCTTCTTCT  1620
   1                            M  I  L  A  N  V  F  C  L  F  F  F   12

1621  TTCTAGACGACACCCTCCGCTCTTTGGCCAGCCCTTCCTCCCTGCAGGGCCCCGAGCTCC  1680
  13   L  D  D  T  L  R  S  L  A  S  P  S  S  L  Q  G  P  E  L  H   32

1681  ACGGCTGGCGCCCCCCAGTGGACTGTGTCCGGGCCAATGAGCTGTGTGCCGCCGAATCCA  1740
  33   G  W  R  P  P  V  D  C  V  R  A  N  E  L  C  A  A  E  S  N   52

1741  ACTGCAGCTCTCGCTACCGCACTCTGCGGCAGTGCCTGGCAGGCCGCGACCGCAACACCA  1800
  53   C  S  S  R  Y  R  T  L  R  Q  C  L  A  G  R  D  R  N  T  M   72

1801  TGCTGGCCAACAAGGAGTGCCAGGCGGCCTTGGAGGTCTTGCAGGAGAGCCCGCTGTACG  1860
  73   L  A  N  K  E  C  Q  A  A  L  E  V  L  Q  E  S  P  L  Y  D   92

1861  ACTGCCGCTGCAAGCGGGGCATGAAGAAGGAGCTGCAGTGTCTGCAGATCTACTGGAGCA  1920
  93   C  R  C  K  R  G  M  K  K  E  L  Q  C  L  Q  I  Y  W  S  I  112

1921  TCCACCTGGGGCTGACCGAGGGTGAGGAGTTCTACGAAGCCTCCCCCTATGAGCCGGTGA  1980
 113   H  L  G  L  T  E  G  E  E  F  Y  E  A  S  P  Y  E  P  V  T  132

1981  CCTCCCGCCTCTCGGACATCTTCAGGCTTGCTTCAATCTTCTCAGGGACAGGGGCAGACC  2040
 133   S  R  L  S  D  I  F  R  L  A  S  I  F  S  G  T  G  A  D  P  152

2041  CGGTGGTCAGCGCCAAGAGCAACCATTGCCTGGATGCTGCCAAGGCCTGCAACCTGAATG  2100
 153   V  V  S  A  K  S  N  H  C  L  D  A  A  K  A  C  N  L  N  D  172

2101  ACAACTGCAAGAAGCTGCGCTCCTCCTACATCTCCATCTGCAACCGCGAGATCTCGCCCA  2160
 173   N  C  K  K  L  R  S  S  Y  I  S  I  C  N  R  E  I  S  P  T  192
```

```
2161  CCGAGCGCTGCAACCGCCGCAAGTGCCACAAGGCCCTGCGCCAGTTCTTCGACCGGGTGC  2220
193    E  R  C  N  R  R  K  C  H  K  A  L  R  Q  F  F  D  R  V  P    212

2221  CCAGCGAGTACACCTACCGCATGCTCTTCTGCTCCTGCCAAGACCAGGCGTGCGCTGAGC  2280
213    S  E  Y  T  Y  R  M  L  F  C  S  C  Q  D  Q  A  C  A  E  R    232

2281  GCCGCCGGCAAACCATCCTGCCCAGCTGCTCCTATGAGGACAAGGAGAAGCCCAACTGCC  2340
233    R  R  Q  T  I  L  P  S  C  S  Y  E  D  K  E  K  P  N  C  L    252

2341  TGGACCTGCGTGGCGTGTGCCGGACTGACCACCTGTGTCGGTCCCGGCTGGCCGACTTCC  2400
253    D  L  R  G  V  C  R  T  D  H  L  C  R  S  R  L  A  D  F  H    272

2401  ATGCCAATTGTCGAGCCTCCTACCAGACGGTCACCAGCTGCCCTGCGGACAATTACCAGG  2460
273    A  N  C  R  A  S  Y  Q  T  V  T  S  C  P  A  D  N  Y  Q  A    292

2461  CGTGTCTGGGCTCTTATGCTGGCATGATTGGGTTTGACATGACACCTAACTATGTGGACT  2520
293    C  L  G  S  Y  A  G  M  I  G  F  D  M  T  P  N  Y  V  D  S    312

2521  CCAGCCCCACTGGCATCGTGGTGTCCCCCTGGTGCAGCTGTCGTGGCAGCGGGAACATGG  2580
313    S  P  T  G  I  V  V  S  P  W  C  S  C  R  G  S  G  N  M  E    332

2581  AGGAGGAGTGTGAGAAGTTCCTCAGGGACTTCACCGAGAACCCATGCCTCCGGAACGCCA  2640
333    E  E  C  E  K  F  L  R  D  F  T  E  N  P  C  L  R  N  A  I    352

2641  TCCAGGCCTTTGGCAACGGCACGAACGTGAACGTGTCCCCAAAAGGCCCCTCGTTCCAGG  2700
353    Q  A  F  G  N  G  T  N  V  N  V  S  P  K  G  P  S  F  Q  A    372

2701  CCACCCAGGCCCCTCGGGTGGAGAAGACGCCTTCTTTGCCAGATGACCTCAGTGACAGTA  2760
373    T  Q  A  P  R  V  E  K  T  P  S  L  P  D  D  L  S  D  S  T    392

2761  CCAGCTTGGGGACCAGTGTCATCACCACCTGCACGTCTGTCCAGGAGCAGGGGCTGAAGG  2820
393    S  L  G  T  S  V  I  T  T  C  T  S  V  Q  E  Q  G  L  K  A    412

2821  CCAACAACTCCAAAGAGTTAAGCATGTGCTTCACAGAGCTCACGACAAATATCATCCCAG  2880
413    N  N  S  K  E  L  S  M  C  F  T  E  L  T  T  N  I  I  P  G    432

2881  GGAGTAACAAGGTGATCAAACCTAACTCAGGCCCCAGCAGAGCCAGACCGTCGGCTGCCT  2940
433    S  N  K  V  I  K  P  N  S  G  P  S  R  A  R  P  S  A  A  L    452

2941  TGACCGTGCTGTCTGTCCTGATGCTGAAACTGGCCTTGTAGGCTGTGGGAACCGAGTCAG  3000
453    T  V  L  S  V  L  M  L  K  L  A  L  *                        464

3001  AAGATTTTTGAAAGCTACGCAGACAAGAACAGCCGCCTGACGAAATGGAAACACACACAG  3060
```

3061 ACACACACACACCTTGCAAAAAAAAAATTGTTTTCCCACCTTGTCGCTGAACCTGTCTC 3120

3121 CTCCCAGGTTTCTTCTCTGGAGAAGTTTTTGTAAACCAAACAGACAAGCAGGCAGGCAGC 3180

3181 CTGAGAGCTGGCCCAGGGGTCCCCTGGCAGGGGAAACTCTGGTGCCGGGGAGGGCACGAG 3240

3241 GCTCTAGAAATGCCCTTCACTTTCTCCTGGTGTTTTTCTCTCTGGACCCTTCTGAAGCAG 3300

3301 AGACCGGACAAGAGCCTGCAGCGGAAGGGACTCTGGGCTGTGCCTGAGGCTGGCTGGGGG 3360

3361 CAGGACAACACAGCTGCTTCCCCAGGCTGCCCACTCTGGGGACCCGCTGGGGGCTGGCAG 3420

3421 AGGGCATCGGTCAGCGGGGCAGCGGGGCTGGCCATGAGGGTCCACCTTCAGCCCTTTGGC 3480

3481 TTCAAGGATGGAGATGGTTTTGCCCTCCCTCTCTGCCCTCGGGTGGGGCTGGTGGGTCTG 3540

3541 CAGCTGGTGTGGGAACTTCCCCACGGATGGCGGTGGAGGGGGTTCGCACCGTGCTGGGCT 3600

3601 CCCCCTGACTGTAGCACGGAGTGTTGGGGCTGGGGGCCAGCTCCAGGAGGGCTTGAGAGC 3660

3661 TCAGCCTGCCTGGGAGAGCCCTTGTGGCGAGGCATTAAAACTTGGGCACCAGCTTCTTTC 3720

3721 TCGGTGGCAGAAATTTTGAAGTCAGAGAGAAACGGTCCTTTGTTGGCTTCTTTGCTTTCT 3780

3781 CGTGGGTCCTTTGGCAGGCCTCCCTTTGGGGAGAGGGAGGGGAGAGACCACAGCCGGGTG 3840

3841 TGTGTCTGCAGCACCGTGGGCCCTCAAGCTTTCCTGCTGTCTTCTCCCTCCTCCTCCTTT 3900

3901 CCCCTTTCTCTTTCCTCATTTCCTAGACGTACGTCAACTGTATGTACATACCGGGGCTCC 3960

3961 TCTCCTAACATATATGTATATACACATCCATATACATATATTGTGTGGTTTCCCCTTTCT 4020

4021 TTCCTTTTTTTAAGCAACAAAACTATGGAAATAATACCCCAACAGATGAGCGAAAATGTA 4080

4081 TTATTGTAAAGTTTATTTTTTTAATACTGTTGTCTATAATGGGGAAAAAGGACATTGGC 4140

4141 CCCGCAGTGCCCTGCCCCAGTCAGCCTGGCTGGGCTCTGGTGGGGGCTCCTGATCCGCAT 4200

4201 CCAAGCTTAACCAAGGCTCCAATAAACGTGCG 4232

Figure 15

Human GRR3

```
  1 CAAGTCAAAGGTTTAATCATGATCCAAGAGCCCAGAGAGACTTTAGGACAATAATAGGAA  60

 61 TAAAGCAAGGCCCACAGGCTCCAGCTCCTGATGCCCAGATGTTCGGCAGGATCCGGGGAC 120

121 AGGGCAGTGCAGGCAGTAGTTTTCCATCCTCCATCCAGGGGAGGAGCGAGGGGAGCGCGG 180

181 AGCCCGGCGCCTACAGCTCGCCATGGTGCGCCCCCTGAACCCGCGACCGCTGCCGCCCGT 240
  1                       M  V  R  P  L  N  P  R  P  L  P  P  V   13

241 AGTCCTGATGTTGCTGCTGCTGCTGCCGCCGTCGCCGCTGCCTCTCGCAGCCGGAGACCC 300
 14  V  L  M  L  L  L  L  L  P  P  S  P  L  P  L  A  A  G  D  P   33

301 CCTTCCCACAGAAAGCCGACTCATGAACAGCTGTCTCCAGGCCAGGAGGAAGTGCCAGGC 360
 34  L  P  T  E  S  R  L  M  N  S  C  L  Q  A  R  R  K  C  Q  A   53

361 TGATCCCACCTGCAGTGCTGCCTACCACCACCTGGATTCCTGCACCTCTAGCATAAGCAC 420
 54  D  P  T  C  S  A  A  Y  H  H  L  D  S  C  T  S  S  I  S  T   73

421 CCCACTGCCCTCAGAGGAGCCTTCGGTCCCTGCTGACTGCCTGGAGGCAGCACAGCAACT 480
 74  P  L  P  S  E  E  P  S  V  P  A  D  C  L  E  A  A  Q  Q  L   93

481 CAGGAACAGCTCTCTGATAGGCTGCATGTGCCACCGGCGCATGAAGAACCAGGTTGCCTG 540
 94  R  N  S  S  L  I  G  C  M  C  H  R  R  M  K  N  Q  V  A  C  113

541 CTTGGACATCTATTGGACCGTTCACCGTGCCCGCAGCCTTGGTAACTATGAGCTGGATGT 600
114  L  D  I  Y  W  T  V  H  R  A  R  S  L  G  N  Y  E  L  D  V  133

601 CTCCCCCTATGAAGACACAGTGACCAGCAAACCCTGGAAAATGAATCTCAGCAAACTGAA 660
134  S  P  Y  E  D  T  V  T  S  K  P  W  K  M  N  L  S  K  L  N  153

661 CATGCTCAAACCAGACTCAGACCTCTGCCTCAAGTTTGCCATGCTGTGTACTCTCAATGA 720
154  M  L  K  P  D  S  D  L  C  L  K  F  A  M  L  C  T  L  N  D  173

721 CAAGTGTGACCGGCTGCGCAAGGCCTACGGGGAGGCGTGCTCCGGGCCCCACTGCCAGCG 780
174  K  C  D  R  L  R  K  A  Y  G  E  A  C  S  G  P  H  C  Q  R  193

781 CCACGTCTGCCTCAGGCAGCTGCTCACTTTCTTCGAGAAGGCCGCCGAGCCCCACGCGCA 840
194  H  V  C  L  R  Q  L  L  T  F  F  E  K  A  A  E  P  H  A  Q  213

841 GGGCCTGCTACTGTGCCCATGTGCCCCCAACGACCGGGGCTGCGGGGAGCGCCGGCGCAA 900
214  G  L  L  L  C  P  C  A  P  N  D  R  G  C  G  E  R  R  R  N  233
```

901 CACCATCGCCCCCAACTGCGCGCTGCCGCCTGTGGCCCCCAACTGCCTGGAGCTGCGGCG 960
234 T I A P N C A L P P V A P N C L E L R R 253

961 CCTCTGCTTCTCCGACCCGCTTTGCAGATCACGCCTGGTGGATTTCCAGACCCACTGCCA 1020
254 L C F S D P L C R S R L V D F Q T H C H 273

1021 TCCCATGGACATCCTAGGAACTTGTGCAACAGAGCAGTCCAGATGTCTACGAGCATACCT 1080
274 P M D I L G T C A T E Q S R C L R A Y L 293

1081 GGGGCTGATTGGGACTGCCATGACCCCCAACTTTGCCAGCAATGTCAACACCAGTGTTGC 1140
294 G L I G T A M T P N F A S N V N T S V A 313

1141 CTTAAGCTGCACCTGCCGAGGCAGTGGCAACCTGCAGGAGGAGTGTGAAATGCTGGAAGG 1200
314 L S C T C R G S G N L Q E E C E M L E G 333

1201 GTTCTTCTCCCACAACCCCTGCCTCACGGAGGCCATTGCAGCTAAGATGCGTTTTCACAG 1260
334 F F S H N P C L T E A I A A K M R F H S 353

1261 CCAACTCTTCTCCCAGGACTGGCCACACCCTACCTTTGCTGTGATGGCACACCAGAATGA 1320
354 Q L F S Q D W P H P T F A V M A H Q N E 373

1321 AAACCCTGCTGTGAGGCCACAGCCCTGGGTGCCCTCTCTTTTCTCCTGCACGCTTCCCTT 1380
374 N P A V R P Q P W V P S L F S C T L P L 393

1381 GATTCTGCTCCTGAGCCTATGGTAGCTGGACTTCCCCAGGGCCCTCTTCCCCTCCACCAC 1440
394 I L L L S L W * 400

1441 ACCCAGGTGGACTTGCAGCCCACAAGGGGTGAGGAAAGGACAGCAGCAGGAAGGAGGTGC 1500

1501 AGTGCGCAGATGAGGGCACAGGAGAAGCTAAGGGTTATGACCTCCAGATCCTTACTGGTC 1560

1561 CAGTCCTCATTCCCTCCACCCCATCTCCACTTCTGATTCATGCTGCCCCTCCTTGGTGGC 1620

1621 CACAATTTAGCCATGTCATCTGGTGGTGACCAGCTCCACCAAGCCCCTTTGTGAGCCCTT 1680

1681 CCTCTTGACTACCAGGATCACCAGAATCTAATAAGTTAGCCTTTCTCTATTGCATTCCAG 1740

1741 ATTAGGGTTAGGGTAGGGAGGACTGGGTGTTCTGAGGCAGCCTAGAAAGTCATTCTCCTT 1800

1801 TGTGAAGAAGGCTCCTGCCCCCTCGTCTCCTCCTCTGAGTGGAGGATGGAAAACTACTGC 1860

1861 CTGCACTGCCCTGTCCCCGGATCCTGCCGAACATCTGGGCATCAGGAGCTGGAGCCTGTG 1920

```
1921   GGCCTTGCTTTATTCCTATTATTGTCCTAAAGTCTCTCTGGGCTCTTGGATCATGATTAA   1980

1981   ACCTTTGACTG   1991
```

Figure 16

Rat GRR2

```
  1  GCGGCCGCGTCGACCTTGACCATGCAGACACTTTTTCAGGCCTCTGTCTGGTGTGAAGTT   60

 61  GGCAGATACAAGCAAGGCCCGAAAGGGGTCTCAGCTTCTCTCTCCTGGGCCTCCTGGACT  120

121  GAGTTAGGCTTGCTTCTGGTTGTCTTCTAAAGGCACGGTGATACAGAATGATGAGACTAG  180

181  GCTGGAGGGGGCTTTCTGCTTCTCTGTGTGTGACCTTGAGTTATCTCCCTTCGTTGGATC  240

241  CGAGCTTTCCTGGAATATGATGTTGAATATGAATATGAGTTCTGCCTAAGGTCCAGACAG  300

301  GCTCTGAGGGTTAACTGACTTTTGGAGCCTTCAAATCAATACCTTGGATGGAGTGGGGGT  360

361  TTGTCCAATGGGAGTTGAGGCAAGATCCCTTTGCATAAGCCTTGCCACATCATGTTGAAG  420

421  CCATGCCATTCTGTCTGGACTATTGGCATCTTACCTTTCCAGCAGTTTCAGTGAAGGCCT  480

481  TCCTGGATTTATCATTCTGTGTTCCACTGCCTAGGATTGTGCTCAAGAGGAAATGAATGT  540

541  GAACCATGGTTGTAGGGGAGTATGGCCAACCAGGTTGGGTCTGTGTTGACCTTGGTCTTG  600
  1      M  V  V  G  E  Y  G  Q  P  G  W  V  C  V  D  L  G  L  G   19

601  GTGTTCTTTTGTGTAAAGTGGGTGAGAAGTTCCTTCAAACCTTAGGCCTACATTGGGGTC  660
 20   V  L  L  C  K  V  G  E  K  F  L  Q  T  L  G  L  H  W  G  Q   39

661  AGAGACTGTGGTGGCCCTCATTCATGCTTGTCTTCCCTTCCCACTACCCAGACGAAACCC  720
 40   R  L  W  W  P  S  F  M  L  V  F  P  S  H  Y  P  D  E  T  L   59

721  TCCGCTCTTTGGCCAGCCCTTCCTCCCTGCAGGGCTCTGAGCTCCACGGCTGGCGCCCCC  780
 60   R  S  L  A  S  P  S  S  L  Q  G  S  E  L  H  G  W  R  P  Q   79

781  AAGTGGACTGTGTCCGGGCCAATGAGCTGTGTGCGGCTGAATCCAACTGCAGCTCCAGGT  840
 80   V  D  C  V  R  A  N  E  L  C  A  A  E  S  N  C  S  S  R  Y   99

841  ACCGCACCCTTCGGCAGTGCCTGGCAGGCCGGGATCGCAATACCATGCTGGCCAATAAGG  900
100   R  T  L  R  Q  C  L  A  G  R  D  R  N  T  M  L  A  N  K  E  119

901  AGTGCCAGGCAGCCCTGGAGGTCTTGCAGGAAAGCCCACTGTATGACTGCCGCTGCAAGC  960
120   C  Q  A  A  L  E  V  L  Q  E  S  P  L  Y  D  C  R  C  K  R  139
```

961 GGGGCATGAAGAAGGAGCTGCAGTGTCTGCAGATCTACTGGAGCATCCATCTGGGGCTGA 1020
140 G M K K E L Q C L Q I Y W S I H L G L T 159

1021 CAGAGGGTGAGGAGTTCTATGAAGCTTCCCCCTATGAGCCTGTGACCTCGCGCCTCTCGG 1080
160 E G E E F Y E A S P Y E P V T S R L S D 179

1081 ACATCTTCAGGCTCGCTTCAATCTTCTCAGGGACAGGGACAGACCCGGCGGTCAGTACCA 1140
180 I F R L A S I F S G T G T D P A V S T K 199

1141 AAAGCAACCACTGCCTGGATGCCGCCAAGGCCTGCAACCTGAATGACAACTGCAAGAAGC 1200
200 S N H C L D A A K A C N L N D N C K K L 219

1201 TTCGCTCCTCTTATATCTCCATCTGCAACCGTGAGATCTCTCCCACCGAACGCTGCAACC 1260
220 R S S Y I S I C N R E I S P T E R C N R 239

1261 GCCGCAAGTGCCACAAGGCTCTGCGCCAGTTCTTTGACCGTGTGCCCAGCGAGTATACCT 1320
240 R K C H K A L R Q F F D R V P S E Y T Y 259

1321 ACCGCATGCTCTTCTGCTCCTGTCAGGACCAGGCATGTGCTGAGCGTCGCCGGCAAACCA 1380
260 R M L F C S C Q D Q A C A E R R R Q T I 279

1381 TCCTGCCCAGTTGCTCCTATGAGGACAAGGAGAAGCCCAACTGCCTGGACCTGCGCAGCC 1440
280 L P S C S Y E D K E K P N C L D L R S L 299

1441 TGTGTCGTACAGACCACCTGTGCCGGTCCCGACTGGCAGATTTCCACGCCAACTGTCGAG 1500
300 C R T D H L C R S R L A D F H A N C R A 319

1501 CCTCCTACCGGACAATCACCAGCTGTCCTGCGGACAACTACCAGGCATGTCTGGGCTCCT 1560
320 S Y R T I T S C P A D N Y Q A C L G S Y 339

1561 ATGCTGGCATGATTGGGTTTGATATGACACCCAACTATGTGGACTCCAACCCCACGGGCA 1620
340 A G M I G F D M T P N Y V D S N P T G I 359

1621 TCGTGGTGTCTCCCTGGTGCAATTGTCGTGGCAGTGGGAACATGGAAGAAGAGTGTGAGA 1680
360 V V S P W C N C R G S G N M E E E C E K 379

1681 AGTTCCTCAGGGACTTCACGGAAAACCCATGCCTCCGGAATGCCATTCAGGCCTTTGGTA 1740
380 F L R D F T E N P C L R N A I Q A F G N 399

1741 ATGGCACAGATGTGAACATGTCTCCCAAAGGCCCCTCACTCCCAGCTACCCAGGCCCCTC 1800
400 G T D V N M S P K G P S L P A T Q A P R 419

1801 GGGTGGAGAAGACTCCTTCACTGCCAGATGACCTCAGTGACAGCACCAGCCTGGGGACCA 1860
420 V E K T P S L P D D L S D S T S L G T S 439

1861 GTGTCATCACCACCTGCACATCTATCCAGGAGCAAGGGCTGAAGGCCAACAACTCCAAAG 1920

```
 440   V  I  T  T  C  T  S  I  Q  E  Q  G  L  K  A  N  N  S  K  E    459

1921  AGTTAAGCATGTGCTTCACAGAGCTCACGACAAACATCAGTCCAGGGAGTAAAAAGGTGA  1980
 460   L  S  M  C  F  T  E  L  T  T  N  I  S  P  G  S  K  K  V  I    479

1981  TCAAACTTAACTCAGGCTCCAGCAGAGCCAGACTGTCGGCTGCCTTGACTGCCCTCCCAC  2040
 480   K  L  N  S  G  S  S  R  A  R  L  S  A  A  L  T  A  L  P  L    499

2041  TCCTGATGCTGACCTTGGCCTTGTAGGCCTTTGGAACCCAGCACAAAAGTTCTTCAAGCA  2100
 500   L  M  L  T  L  A  L  *                                         506

2101  ACCCAGATATGAACTCCCGCCTGACAAAATGGAAACACACGCATACACACATGCCACACA  2160

2161  CAGACACACACACAGACACACACACACACACATACAGACGTCGACGCGGCCGC  2215
```

Figure 17

Rat GRR3

```
  1 GCGGCCGCGTCGACCGACGCCCAGCACAGGCAGAGCGCTGCCGGGTCCGCGGCGTCCAGA  60

 61 CCCGCCATGGGGCTCTCCCGGAGCCCGCGACCGCCGCCGCTAGTGATCCTGCTACTGGTG 120
  1       M  G  L  S  R  S  P  R  P  P  P  L  V  I  L  L  L  V   18

121 CTGTCGCTGTGGCTACCCCTTGGAACAGGAAACTCCCTTCCCACAGAGAACAGGCTTGTG 180
 19 L  S  L  W  L  P  L  G  T  G  N  S  L  P  T  E  N  R  L  V   38

181 AACAGCTGTACCCAGGCCAGAAAAAAATGCGAGGCTAATCCCGCTTGCAAGGCTGCCTAC 240
 39 N  S  C  T  Q  A  R  K  K  C  E  A  N  P  A  C  K  A  A  Y   58

241 CAGCACCTGGACTCCTGCACCCCCAGTCTCAGCAGTCCACTGCCCTCAGGGGAGTCTGCC 300
 59 Q  H  L  D  S  C  T  P  S  L  S  S  P  L  P  S  G  E  S  A   78

301 ACATCTGCAGCGTGCCTTGAAGCAGCACAGCAACTCAGGAACAGCTCTCTCATAGACTGC 360
 79 T  S  A  A  C  L  E  A  A  Q  Q  L  R  N  S  S  L  I  D  C   98

361 AGGTGCCACCGGCGCATGAAGCACCAAGCTACCTGTCTGGACATTTATTGGACCGTTCAC 420
 99 R  C  H  R  R  M  K  H  Q  A  T  C  L  D  I  Y  W  T  V  H  118

421 CCTGTCCGAAGCCTTGGTGACTACGAGTTGGACGTCTCACCCTATGAAGACACAGTGACC 480
119 P  V  R  S  L  G  D  Y  E  L  D  V  S  P  Y  E  D  T  V  T  138

481 AGCAAACCCTGGAAAATGAATCTCAGCAAGCTGAGCATGCTCAAACCAGACTCCGACCTC 540
139 S  K  P  W  K  M  N  L  S  K  L  S  M  L  K  P  D  S  D  L  158

541 TGCCTCAAATTTGCTATGCTGTGTACTCTTAACGACAAGTGCGACCGCCTCCGAAAGGCC 600
159 C  L  K  F  A  M  L  C  T  L  N  D  K  C  D  R  L  R  K  A  178

601 TACGGGGAGGCGTGCTCAGGGATCCGCTGCCAGCGCCACCTCTGCCTAGCTCAGCTGCGC 660
179 Y  G  E  A  C  S  G  I  R  C  Q  R  H  L  C  L  A  Q  L  R  198

661 TCCTTCTTCGAGAAGGCGGCAGAGTCCCACGCTCAGGGCCTGCTGCTGTGTCCCTGTGCA 720
199 S  F  F  E  K  A  A  E  S  H  A  Q  G  L  L  L  C  P  C  A  218

721 CCCGAAGATGCGGGCTGTGGGGAGCGCCGGCGCAACACCATCGCCCCCAGTTGCGCCCTC 780
219 P  E  D  A  G  C  G  E  R  R  R  N  T  I  A  P  S  C  A  L  238

781 CCGTCTGTGGCCCCCAACTGCCTAGATCTTCGGAGCTTCTGCCGTGCGGACCCTCTGTGC 840
239 P  S  V  A  P  N  C  L  D  L  R  S  F  C  R  A  D  P  L  C  258
```

841 AGATCACGCCTGATGGACTTCCAGACCCACTGCCACCCTATGGACATCCTCGGGACTTGT 900
259 R S R L M D F Q T H C H P M D I L G T C 278

901 GCAACTGAGCAGTCCAGATGTCTGCGGGCATACCTGGGGCTAATTGGGACTGCCATGACC 960
279 A T E Q S R C L R A Y L G L I G T A M T 298

961 CCAAACTTCATCAGCAAGGTCAACACTACTGTTGCCTTAGGCTGTACCTGCCGAGGCAGT 1020
299 P N F I S K V N T T V A L G C T C R G S 318

1021 GGCAACCTGCAGGACGAGTGTGAACAGCTGGAAAAGTCCTTCTCCCAGAACCCCTGCCTC 1080
319 G N L Q D E C E Q L E K S F S Q N P C L 338

1081 ATGGAGGCCATTGCGGCTAAAATGCGTTTCCACAGACAACTCTTCTCCCAGGACTGGGCG 1140
339 M E A I A A K M R F H R Q L F S Q D W A 358

1141 GACTCTACTTTTTCTGTGATGCAGCAGCAGAACAGCAGCCCTGCTCTGAGGCCCCAGCTC 1200
359 D S T F S V M Q Q Q N S S P A L R P Q L 378

1201 AGGCTACCCGTTCTGTCTTTCTTCATCCTTACCTTGATTCTGCTGCAGACCCTCTGGTAA 1260
379 R L P V L S F F I L T L I L L Q T L W * 397

1261 CTGGGCTCCCTCAGGGTCCTTTGTCCTCTCCACCACACCCAGACCGACTTGCAGCCTGTG 1320

1321 ATGGGAGAGAAAATGCTGGCCTCTGGAAGAAGATGCAACCAGGCTCACTGCACATCCTGT 1380

1381 CTGCTCCAGATGAGGTCTTGGAAGAAGCGAGGGCTGTGACCGTTCAGAATCCTGAGCGGC 1440

1441 CAGCTTTCAAACCTCTCCTACTTACTCCTGCTTGGGCTGCTCCTCCCTAGGACCTTGTAC 1500

1501 TCCAGTTTGGCTGTATATTGTGGTGGTGATTAGCTTCCCACCTCCAGCCCTTCTTCCTGT 1560

1561 TTCCCAGGACCACCCAGGGCTAATGACTCACTCATTCCTGGTTGCCTTCTCCAGGAAGGC 1620

1621 AGGCTGAGGGTTCTGAGGCAGCTGAGAAAGATGGTCCCTTTGTGAGGAAGGCTGGTGGTC 1680

1681 CAACCGTCGACGCGGCCGC 1699

Figure 18

Alignment of the Amino Acid Sequeces of GDNFRs

1					50
Mgdnfr	~~~~~~~~~~	~~~~MFLATL	YFVLPLLDLL	MSAEVSG.GD	RLDCVKASDQ
Rgdnfr	~~~~~~~~~~	~~~~MFLATL	YFALPLLDLL	MSAEVSG.GD	RLDCVKASDQ
Hgdnfr	~~~~~~~~~~	~~~~MFLATL	YFALPLLDLL	LSAEVSG.GD	RLDCVKASDQ
Hgrr2	~~~~MILANV	FCLFFFLDDT	LRSLASPSSL	QGPELHGWRP	PVDCVRANEL
Rgrr2	~~~~~~~~ML	VFPSHYPDET	LRSLASPSSL	QGSELHGWRP	QVDCVRANEL
Hgrr3	MVRPLNPRPL	PPVVLMLLLL	LPPSPLPLAA	GDPLPTESRL	MNSCLQARRK
Rgrr3	MGLSRSPRPP	PLVILLLVLS	L...WLPLGT	GNSLPTENRL	VNSCTQARKK

	51				100
Mgdnfr	CLKEQSCSTK	YRTLRQCVAG	KETNFSLTSG	LEAKDECRSA	MEALKQKSLY
Rgdnfr	CLKEQSCSTK	YRTLRQCVAG	KETNFSLTSG	LEAKDECRSA	MEALKQKSLY
Hgdnfr	CLKEQSCSTK	YRTLRQCVAG	KETNFSLASG	LEAKDECRSA	MEALKQKSLY
Hgrr2	CAAESNCSSR	YRTLRQCLAG	RDRNTML...	..ANKECQAA	LEVLQESPLY
Rgrr2	CAAESNCSSR	YRTLRQCLAG	RDRNTML...	..ANKECQAA	LEVLQESPLY
Hgrr3	CQADPTCSAA	YHHLDSCTSS	ISTPLP.SEE	PSVPADCLEA	AQQLRNSSLI
Rgrr3	CEANPACKAA	YQHLDSCTPS	LSSPLP.SGE	SATSAACLEA	AQQLRNSSLI

	101				150
Mgdnfr	NCRCKRGMKK	EKNCLRIYWS	MYQSL.QGND	LLEDSPYEPV	NSRLSDIFRA
Rgdnfr	NCRCKRGMKK	EKNCLRIYWS	MYQSL.QGND	LLEDSPYEPV	NSRLSDIFRA
Hgdnfr	NCRCKRGMKK	EKNCLRIYWS	MYQSL.QGND	LLEDSPYEPV	NSRLSDIFRV
Hgrr2	DCRCKRGMKK	ELQCLQIYWS	IHLGLTEGEE	FYEASPYEPV	TSRLSDIFRL
Rgrr2	DCRCKRGMKK	ELQCLQIYWS	IHLGLTEGEE	FYEASPYEPV	TSRLSDIFRL
Hgrr3	GCMCHRRMKN	QVACLDIYWT	VHRARSLGNY	ELDVSPYE..	.....DTVTS
Rgrr3	DCRCHRRMKH	QATCLDIYWT	VHPVRSLGDY	ELDVSPYE..	.....DTVTS

	151				200
Mgdnfr	VPFISDVFQQ	VEHISKGNNC	LDAAKACNLD	DTCKKYRSAY	ITPCTTSMS.
Rgdnfr	VPFISDVFQQ	VEHISKGNNC	LDAAKACNLD	DTCKKYRSAY	ITPCTTSMS.
Hgdnfr	VPFISDVFQQ	VEHIPKGNNC	LDAAKACNLD	DICKKYRSAY	ITPCTTSVS.
Hgrr2	ASIFSGTGAD	PVVSAKSNHC	LDAAKACNLN	DNCKKLRSSY	ISICNREISP
Rgrr2	ASIFSGTGTD	PAVSTKSNHC	LDAAKACNLN	DNCKKLRSSY	ISICNREISP
Hgrr3	KPWKMNLSKL	NMLKPDSDLC	LKFAMLCTLN	DKCDRLRKAY	GEACS.....

Rgrr3	KPWKMNLSKL	SMLKPDSDLC	LKFAMLCTLN	DKCDRLRKAY	GEACS.....

	201				250
Mgdnfr	NEVCNRRKCH	KALRQFFDKV	PAKHSYGMLF	CSC..RDVAC	TERRRQTIVP
Rgdnfr	NEVCNRRKCH	KALRQFFDKV	PAKHSYGMLF	CSC..RDIAC	TERRRQTIVP
Hgdnfr	NDVCNRRKCH	KALRQFFDKV	PAKHSYGMLF	CSC..RDIAC	TERRRQTIVP
Hgrr2	TERCNRRKCH	KALRQFFDRV	PSEYTYRMLF	CSC..QDQAC	AERRRQTILP
Rgrr2	TERCNRRKCH	KALRQFFDRV	PSEYTYRMLF	CSC..QDQAC	AERRRQTILP
Hgrr3	GPHCQRHVCL	RQLLTFFEKA	AEPHAQGLLL	CPCAPNDRGC	GERRRNTIAP
Rgrr3	GIRCQRHLCL	AQLRSFFEKA	AESHAQGLLL	CPCAPEDAGC	GERRRNTIAP

```
        251                                                  300
Mgdnfr  VCSYEERERP NCLNLQDSCK TNYICRSRLA DFFTNCQPES RSVSNCLKEN
Rgdnfr  VCSYEERERP NCLSLQDSCK TNYICRSRLA DFFTNCQPES RSVSNCLKEN
Hgdnfr  VCSYEEREKP NCLNLQDSCK TNYICRSRLA DFFTNCQPES RSVSSCLKEN
 Hgrr2  SCSYEDKEKP NCLDLRGVCR TDHLCRSRLA DFHANCRASY QTVTSCPADN
 Rgrr2  SCSYEDKEKP NCLDLRSLCR TDHLCRSRLA DFHANCRASY RTITSCPADN
 Hgrr3  NCALPP.VAP NCLELRRLCF SDPLCRSRLV DFQTHCHP.. MDILGTCATE
 Rgrr3  SCALPS.VAP NCLDLRSFCR ADPLCRSRLM DFQTHCHP.. MDILGTCATE

        301                                                  350
Mgdnfr  YADCLLAYSG LIGTVMTPNY VDSS..SLSV APWCDCSNSG NDLEDCLKFL
Rgdnfr  YADCLLAYSG LIGTVMTPNY VDSS..SLSV APWCDCSNSG NDLEDCLKFL
Hgdnfr  YADCLLAYSG LIGTVMTPNY IDSS..SLSV APWCDCSNSG NDLEECLKFL
 Hgrr2  YQACLGSYAG MIGFDMTPNY VDSSPTGIVV SPWCSCRGSG NMEEECEKFL
 Rgrr2  YQACLGSYAG MIGFDMTPNY VDSNPTGIVV SPWCNCRGSG NMEEECEKFL
 Hgrr3  QSRCLRAYLG LIGTAMTPNF ASNVNTSVAL S..CTCRGSG NLQEECEMLE
 Rgrr3  QSRCLRAYLG LIGTAMTPNF ISKVNTTVAL G..CTCRGSG NLQDECEQLE

        351                                                  400
Mgdnfr  NFFKDNTCLK NAIQAFGNGS DVTMWQPAP. PVQTTTATTT TAFRIKNKPS
Rgdnfr  NFFKDNTCLK NAIQAFGNGS DVTMWQPAP. PVQTTTATTT TAFRVKNKPL
Hgdnfr  NFFKDNTCLK NAIQAFGNGS DVTVWQPAF. PVQTTTATTT TALRVKNKPL
 Hgrr2  RDFTENPCLR NAIQAFGNGT NVNVSPKGP. SFQATQAPRV EKTPSLPDDL
 Rgrr2  RDFTENPCLR NAIQAFGNGT DVNMSPKGP. SLPATQAPRV EKTPSLPDDL
 Hgrr3  GFFSHNPCLT EAIAAKMRFH SQLFSQDWPH PTFAVMAHQN ENPAVRPQPW
 Rgrr3  KSFSQNPCLM EAIAAKMRFH RQLFSQDWAD STFSVMQQQN SSPALRPQLR

        401                                                  450
Mgdnfr  GPACSENEIP THVLPPCANL QAQKLKSNVS GSTHLCLSDN DYGKDGLAGA
Rgdnfr  GPAGSENEIP THVLPPCANL QAQKLKSNVS GSTHLCLSDS DFGKDGLAGA
Hgdnfr  GPAGSENEIP THVLPPCANL QAQKLKSNVS GNTHLCISNG NYEKEGL.GA
 Hgrr2  SDSTS...LG TSVITTCTSV QEQGLKANNS KELSMCFTEL TTNIIPGSNK
 Rgrr2  SDSTS...LG TSVITTCTSI QEQGLKANNS KELSMCFTEL TTNISPGSKK
 Hgrr3  VPSLFSCTLP LILLLSLW~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
 Rgrr3  LPVLSFFILT LILLQTLW*~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
```

```
        451                                      490
Mgdnfr  SSHITTKSMA APPSCGLSSL PVMVFTALAA LLSVSLAETS
Rgdnfr  SSHITTKSMA APPSCSLSSL PVLMLTALAA LLSVSLAETS
Hgdnfr  SSHITTKSMA APPSCGLSPL LVLVVTALST LLSLTETS~~
 Hgrr2  VIKPNSGPSR ARPSAALTVL SVLMLKLAL* ~~~~~~~~~~
 Rgrr2  VIKLNSGSSR ARLSAALTAL PLLMLTLAL* ~~~~~~~~~~
 Hgrr3  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
 Rgrr3  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
```

Figure 19

GDNFR Family of Receptors

	1				50
Consensus	MV..l...p	.pp...m.l.	llslalPl..	.lqgael.g.	.Rl..dCv.A.
Hgdnfr		MFLAT	LYFALPLLDL	LLSAEVSGGD	RL..DCVKAS
Rgdnfr		MFLAT	LYFALPLLDL	LMSAEVSGGD	RL..DCVKAS
Hgrr2	MILANVF	CLFFFLDDTL	RSLASPSS..	LQGPELHGW.	RPPVDCVRAN
Rgrr2	MLV	FPSHYPDETL	RSLASPSS..	LQGSELHGW.	RPQVDCVRAN
Hgrr3	MVRPLNPRPL	PPVVLMLLLL	LPPS.PLP.L	AAGDPLPTES	RLMNSCLQAR
Rgrr3	MGLSRSPR	PPPLVILLLV	LSLWLPLG..	.TGNSLPTEN	RLVNSCTQAR

	51				100
Consensus	..C.ae..Cs	..YrtLrqC.	ag...nt.La	sg.E......	C..A.e.L..
Hgdnfr	DQCLKEQSCS	TKYRTLRQCV	AGKETNFSLA	SGLEAKDE..	CRSAMEALKQ
Rgdnfr	DQCLKEQSCS	TKYRTLRQCV	AGKETNFSLT	SGLEAKDE..	CRSAMEALKQ
Hgrr2	ELCAAESNCS	SRYRTLRQCL	AGRDRNTMLA	NK.E......	CQAALEVLQE
Rgrr2	ELCAAESNCS	SRYRTLRQCL	AGRDRNTMLA	NK.E......	CQAALEVLQE
Hgrr3	RKCQADPTCS	AAYHHLDSCT	..SSISTPLP	SE.EPSVPAD	CLEAAQQLRN
Rgrr3	KKCEANPACK	AAYQHLDSCT	..PSLSSPLP	SG.ESATSAA	CLEAAQQLRN

	101				150
Consensus	ssLydCrCkR	gMKke..CL.	IYWs.h..l.	.Gn..le.SP	YEp.VtSrls
Hgdnfr	KSLYNCRCKR	GMKKEKNCLR	IYWSMYQSLQ	.GNDLLEDSP	YEP.VNSRLS
Rgdnfr	KSLYNCRCKR	GMKKEKNCLR	IYWSMYQSLQ	.GNDLLEDSP	YEP.VNSRLS
Hgrr2	SPLYDCRCKR	GMKKELQCLQ	IYWSIHLGLT	EGEEFYEASP	YEP.VTSRLS
Rgrr2	SPLYDCRCKR	GMKKELQCLQ	IYWSIHLGLT	EGEEFYEASP	YEP.VTSRLS
Hgrr3	SSLIGCMCHR	RMKNQVACLD	IYWTVHRARS	LGNYELDVSP	YEDTVTSKPW
Rgrr3	SSLIDCRCHR	RMKHQATCLD	IYWTVHPVRS	LGDYELDVSP	YEDTVTSKPW

```
             151                                                    200
Consensus    difr..s..s ....d..... ksn.CLdaAk aCnLnD.Ckk lRsaYi..C.
   Hgdnfr    DIFRVVPFIS DVFQQVEHIP KGNNCLDAAK ACNLDDICKK YRSAYITPCT
   Rgdnfr    DIFRAVPFIS DVFQQVEHIS KGNNCLDAAK ACNLDDTCKK YRSAYITPCT
    Hgrr2    DIFRLASIFS GTGADPVVSA KSNHCLDAAK ACNLNDNCKK LRSSYISICN
    Rgrr2    DIFRLASIFS GTGTDPAVST KSNHCLDAAK ACNLNDNCKK LRSSYISICN
    Hgrr3    KMNL..SKLN MLKPD..... .SDLCLKFAM LCTLNDKCDR LRKAYGEAC.
    Rgrr3    KMNL..SKLS MLKPD..... .SDLCLKFAM LCTLNDKCDR LRKAYGEAC.

             201                                                    250
Consensus    ...S..erCn RrkChkaLrq FFdkvp..h. ygmLfCsC.. .D.aC.ERRR
   Hgdnfr    TSVS.NDVCN RRKCHKALRQ FFDKVPAKHS YGMLFCSC.. RDIACTERRR
   Rgdnfr    TSMS.NEVCN RRKCHKALRQ FFDKVPAKHS YGMLFCSC.. RDIACTERRR
    Hgrr2    REISPTERCN RRKCHKALRQ FFDRVPSEYT YRMLFCSC.. QDQACAERRR
    Rgrr2    REISPTERCN RRKCHKALRQ FFDRVPSEYT YRMLFCSC.. QDQACAERRR
    Hgrr3    ...SG.PHCQ RHVCLRQLLT FFEKAAEPHA QGLLLCPCAP NDRGCGERRR
    Rgrr3    ...SG.IRCQ RHLCLAQLRS FFEKAAESHA QGLLLCPCAP EDAGCGERRR

             251                                                    300
Consensus    qTI.PsCsye ..ekPNCLdL r..Crtd.lC RSRLaDF.tn C....r.v.s
   Hgdnfr    QTIVPVCSYE EREKPNCLNL QDSCKTNYIC RSRLADFFTN CQPESRSVSS
   Rgdnfr    QTIVPVCSYE ERERPNCLSL QDSCKTNYIC RSRLADFFTN CQPESRSVSN
    Hgrr2    QTILPSCSYE DKEKPNCLDL RGVCRTDHLC RSRLADFHAN CRASYQTVTS
    Rgrr2    QTILPSCSYE DKEKPNCLDL RSLCRTDHLC RSRLADFHAN CRASYRTITS
    Hgrr3    NTIAPNC.AL PPVAPNCLEL RRLCFSDPLC RSRLVDFQTH C.HPMDILGT
    Rgrr3    NTIAPSC.AL PSVAPNCLDL RSFCRADPLC RSRLMDFQTH C.HPMDILGT

             301                                                    350
Consensus    C.a.ny..CL .aY.GlIGt. MTPNyvdss. t...VapwC. CrgSGN..ee
   Hgdnfr    CLKENYADCL LAYSGLIGTV MTPNYIDSSS ..LSVAPWCD CSNSGNDLEE
   Rgdnfr    CLKENYADCL LAYSGLIGTV MTPNYVDSSS ..LSVAPWCD CSNSGNDLED
    Hgrr2    CPADNYQACL GSYAGMIGFD MTPNYVDSSP TGIVVSPWCS CRGSGNMEEE
    Rgrr2    CPADNYQACL GSYAGMIGFD MTPNYVDSNP TGIVVSPWCN CRGSGNMEEE
    Hgrr3    C.ATEQSRCL RAYLGLIGTA MTPNFASNVN TS..VALSCT CRGSGNLQEE
    Rgrr3    C.ATEQSRCL RAYLGLIGTA MTPNFISKVN TT..VALGCT CRGSGNLQDE
```

```
             351                                                400
Consensus    Cekfl.fF.. NpCL.nAIqA fgng...... .....p.fsv .....t.t.a
   Hgdnfr    CLKFLNFFKD NTCLKNAIQA FGNGS....D VTVWQPAFPV QTTTATTTTA
   Rgdnfr    CLKFLNFFKD NTCLKNAIQA FGNGS....D VTMWQPAPPV QTTTATTTTA
    Hgrr2    CEKFLRDFTE NPCLRNAIQA FGNGTNV... ......NVSP KGPSFQATQA
    Rgrr2    CEKFLRDFTE NPCLRNAIQA FGNGTDV... ......NMSP KGPSLPATQA
    Hgrr3    CEMLEGFFSH NPCLTEAIAA KMRFHSQLFS QDWPHPTFAV MAHQNENPAV
    Rgrr3    CEQLEKSFSQ NPCLMEAIAA KMRFHRQLFS QDWADSTFSV MQQQNSSPAL

             401                                                450
Consensus    .rv...PsL. ...s....l. t.v...C..l Q.Q.LK.N.S .e...Cf.el
   Hgdnfr    LRVKNKP.LG PAGSENEIP. THVLPPCANL QAQKLKSNVS GNTHLCISNG
   Rgdnfr    FRVKNKP.LG PAGSENEIP. THVLPPCANL QAQKLKSNVS GSTHLCLSDS
    Hgrr2    PRVEKTPSLP DDLSDSTSLG TSVITTCTSV QEQGLKANNS KELSMCFTEL
    Rgrr2    PRVEKTPSLP DDLSDSTSLG TSVITTCTSI QEQGLKANNS KELSMCFTEL
    Hgrr3    RPQPWVPSLF SCTLPLILLL SLW
    Rgrr3    RPQLRLPVLS FFILTLILLQ TLW

             451                                               499
Consensus    ttn....sg. ...i...s.. A.pS.aL..L pvlmltala. LLS....S
   Hgdnfr    NYEKEGL.GA SSHITTKSMA APPSCGLSPL LVRVVTALST LLSLTETS
   Rgdnfr    DFGKDGLAGA SSHITTKSMA APPSCSLSSL PVLMLTALAA LLSVSLA
    Hgrr2    TTNIIPGSNK VIKPNSGPSR ARPSAALTVL SVLMLK.LAL
    Rgrr2    TTNISPGSKK VIKLNSGSSR ARLSAALTAL PLLMLTLAL
```

Figure 20

```
Human GDNFRα                MFLATLYFALPLLDLLLSAEVSGGDRLDCVKASDQCLKE
Rat GDNFRα                  MFLATLYFALPLLDLLMSAEVSGGDRLDCVKASDQCLKE
Human GRR2    MILANVFCLFFFLDDTLRSLASPSSLQGPELHGWRPPVDCVRANELCAAE
Rat GRR2         MLVFPSHYPDETLRSLASPSSLQGSELHGWRPQVDCVRANELCAAE

Human GDNFRα  QSCSTKYRTLRQCVAGKETNFSLASGLEAKDECRSAMEALKQKSLYNCRC
Rat GDNFRα    QSCSTKYRTLRQCVAGKETNFSLTSGLEAKDECRSAMEALKQKSLYNCRC
Human GRR2    SNCSSRYRTLRQCLAGRDRN.....TMLANKECQAALEVLQESPLYDCRC
Rat GRR2      SNCSSRYRTLRQCLAGRDRN.....TMLANKECQAALEVLQESPLYDCRC

Human GDNFRα  KRGMKKEKNCLRIYWSMYQSL.QGNDLLEDSPYEPVNSRLSDIFRVVPFI
Rat GDNFRα    KRGMKKEKNCLRIYWSMYQSL.QGNDLLEDSPYEPVNSRLSDIFRAVPFI
Human GRR2    KRGMKKELQCLQIYWSIHLGLTEGEEFYEASPYEPVTSRLSDIFRLASIF
Rat GRR2      KRGMKKELQCLQIYWSIHLGLTEGEEFYEASPYEPVTSRLSDIFRLASIF

Human GDNFRα  SDVFQQVEHIPKGNNCLDAAKACNLDDICKKYRSAYITPCTTSVS.NDVC
Rat GDNFRα    SDVFQQVEHISKGNNCLDAAKACNLDDTCKKYRSAYITPCTTSMS.NEVC
Human GRR2    SGTGADPVVSAKSNHCLDAAKACNLNDNCKKLRSSYISICNREISPTERC
Rat GRR2      SGTGTDPAVSTKSNHCLDAAKACNLNDNCKKLRSSYISICNREISPTERC

Human GDNFRα  NRRKCHKALRQFFDKVPAKHSYGMLFCSCRDIACTERRRQTIVPVCSYEE
Rat GDNFRα    NRRKCHKALRQFFDKVPAKHSYGMLFCSCRDIACTERRRQTIVPVCSYEE
Human GRR2    NRRKCHKALRQFFDRVPSEYTYRMLFCSCQDQACAERRRQTILPSCSYED
Rat GRR2      NRRKCHKALRQFFDRVPSEYTYRMLFCSCQDQACAERRRQTILPSCSYED

Human GDNFRα  REKPNCLNLQDSCKTNYICRSRLADFFTNCQPESRSVSSCLKENYADCLL
Rat GDNFRα    RERPNCLSLQDSCKTNYICRSRLADFFTNCQPESRSVSNCLKENYADCLL
Human GRR2    KEKPNCLDLRGVCRTDHLCRSRLADFHANCRASYQTVTSCPADNYQACLG
Rat GRR2      KEKPNCLDLRSLCRTDHLCRSRLADFHANCRASYRTITSCPADNYQACLG

Human GDNFRα  AYSGLIGTVMTPNYIDSS..SLSVAPWCDCSNSGNDLEECLKFLNFFKDN
Rat GDNFRα    AYSGLIGTVMTPNYVDSS..SLSVAPWCDCSNSGNDLEDCLKFLNFFKDN
Human GRR2    SYAGMIGFDMTPNYVDSSPTGIVVSPWCSCRGSGNMEEECEKFLRDFTEN
Rat GRR2      SYAGMIGFDMTPNYVDSNPTGIVVSPWCNCRGSGNMEEECEKFLRDFTEN

Human GDNFRα  TCLKNAIQAFGNGSDVTVWQPAFPVQTTTATTTTALRVKNKPLGPAGSEN
Rat GDNFRα    TCLKNAIQAFGNGSDVTMWQPAPPVQTTTATTTTAFRVKNKPLGPAGSEN
Human GRR2    PCLRNAIQAFGNGTNVNVSPKGPSFQATQAPRVEKTPSLPDDLSDSTS..
Rat GRR2      PCLRNAIQAFGNGTDVNMSPKGPSLPATQAPRVEKTPSLPDDLSDSTS..

Human GDNFRα  EIPTHVLPPCANLQAQKLKSNVSGNTHLCISNGNYEKEGL.GASSHITTK
Rat GDNFRα    EIPTHVLPPCANLQAQKLKSNVSGSTHLCLSDSDFGKDGLAGASSHITTK
Human GRR2    .LGTSVITTCTSVQEQGLKANNSKELSMCFTELTTNIIPGSNKVIKPNSG
Rat GRR2      .LGTSVITTCTSIQEQGLKANNSKELSMCFTELTTNISPGSKKVIKLNSG

Human GDNFRα  SMAAPPSCGLSPLLVLVVT.ALSTLL..SLTETS
Rat GDNFRα    SMAAPPSCSLSSLPVLMLT.ALAALLSVSLAETS
Human GRR2    PSRARPSAALTVLSVLMLKLAL
Rat GRR2      SSRARLSAALTALPLLMLTLAL
```

Figure 21

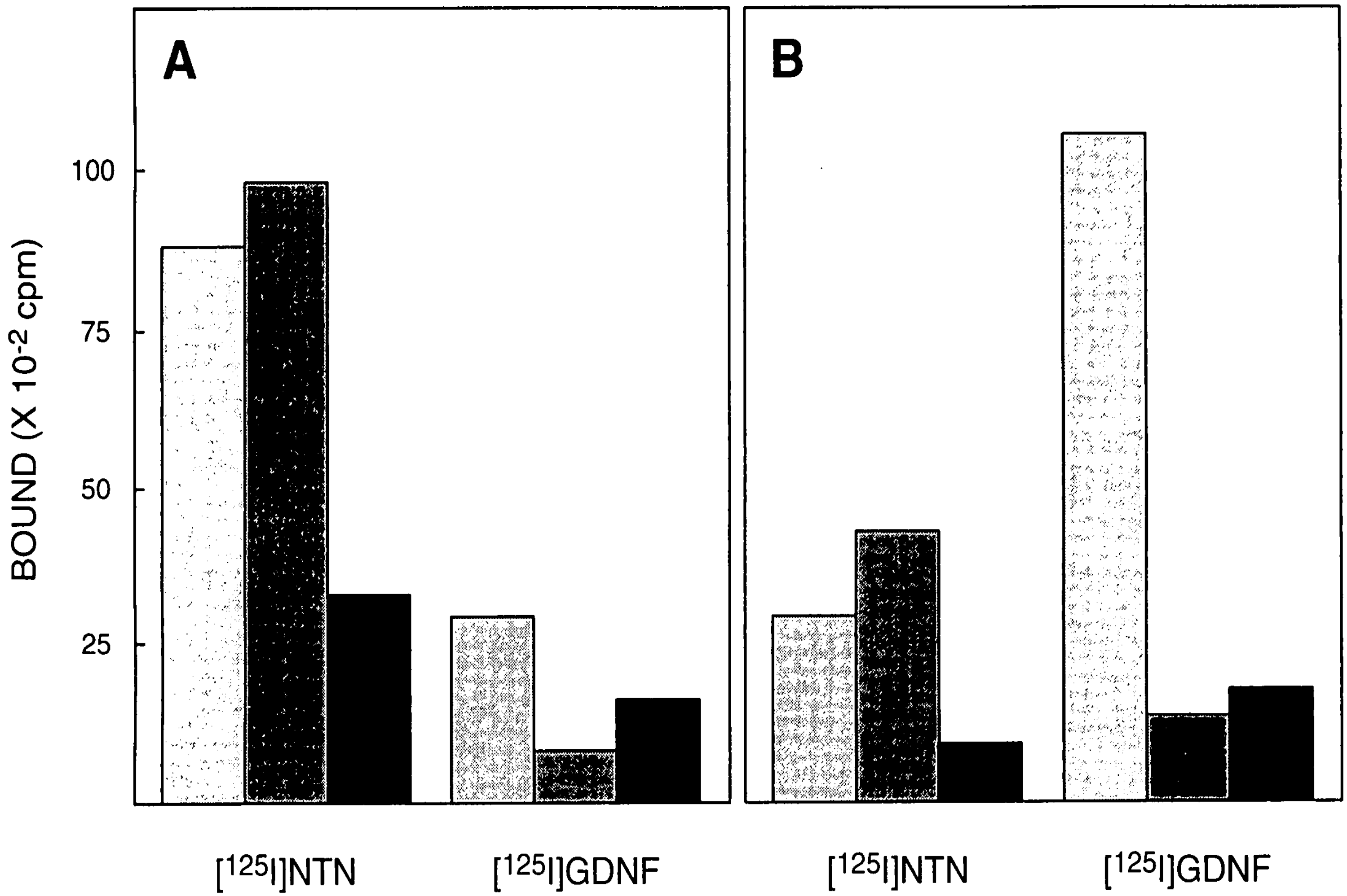

A
B
BOUND (X 10-2 cpm)
100
75
50
25
[125I]NTN
[125I]GDNF
[125I]NTN
[125I]GDNF

Figure 22

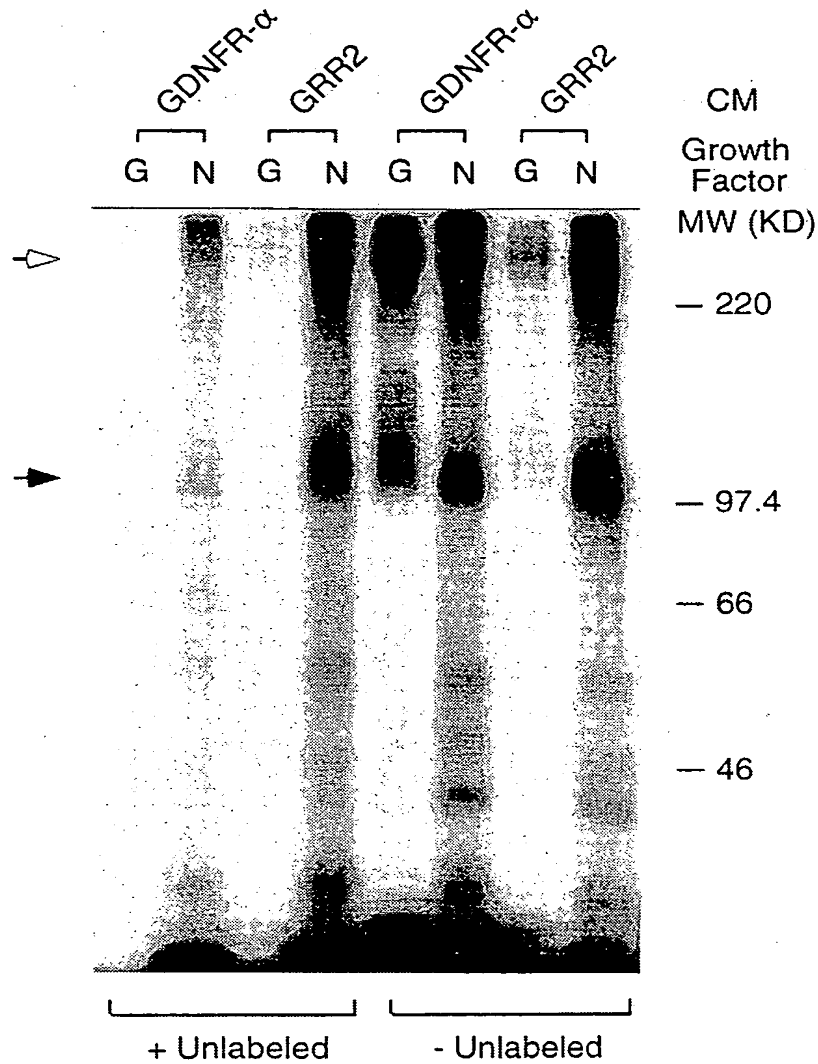

GDNFR-α
GRR2
GDNFR-α
GRR2
CM
G N G N G N G N
Growth Factor
MW (KD)
— 220
— 97.4
— 66
— 46
+ Unlabeled
- Unlabeled

Figure 23

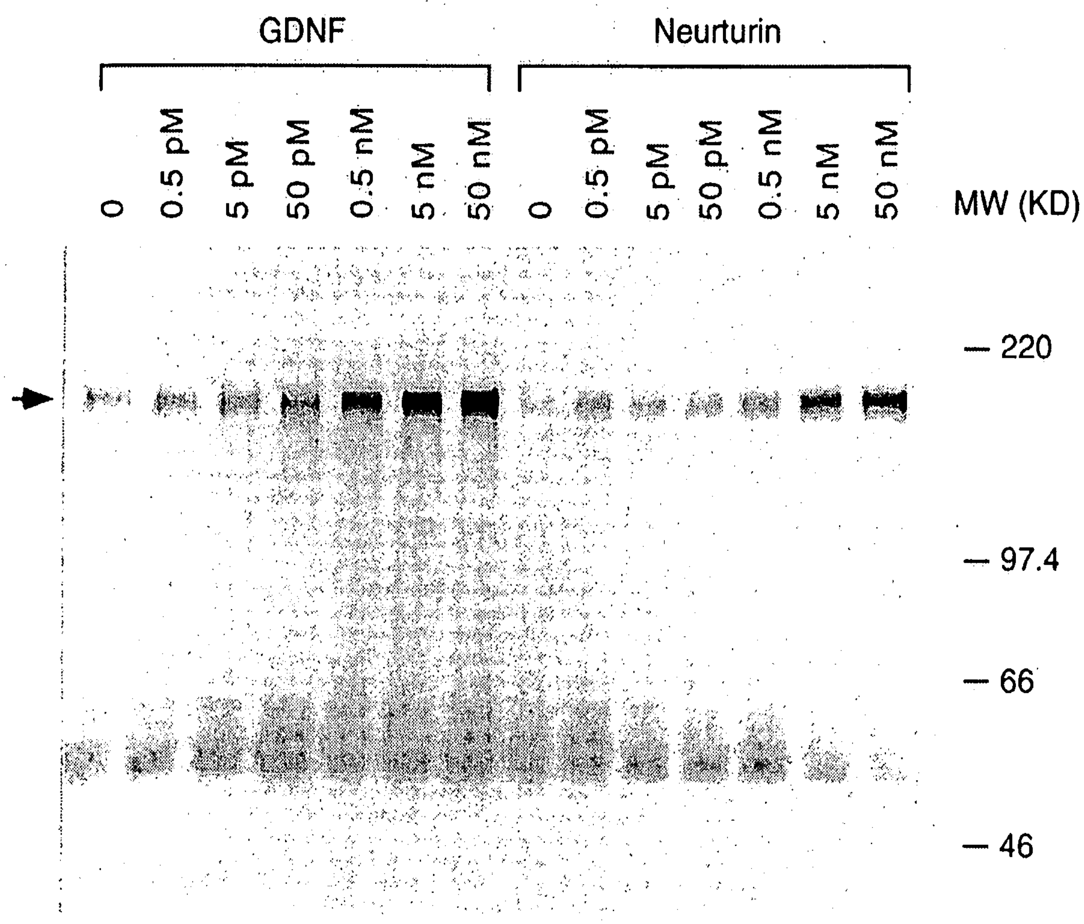

GDNF
Neurturin
0
0.5 pM
5 pM
50 pM
0.5 nM
5 nM
50 nM
0
0.5 pM
5 pM
50 pM
0.5 nM
5 nM
50 nM
MW (KD)
— 220
— 97.4
— 66
— 46

Figure 24

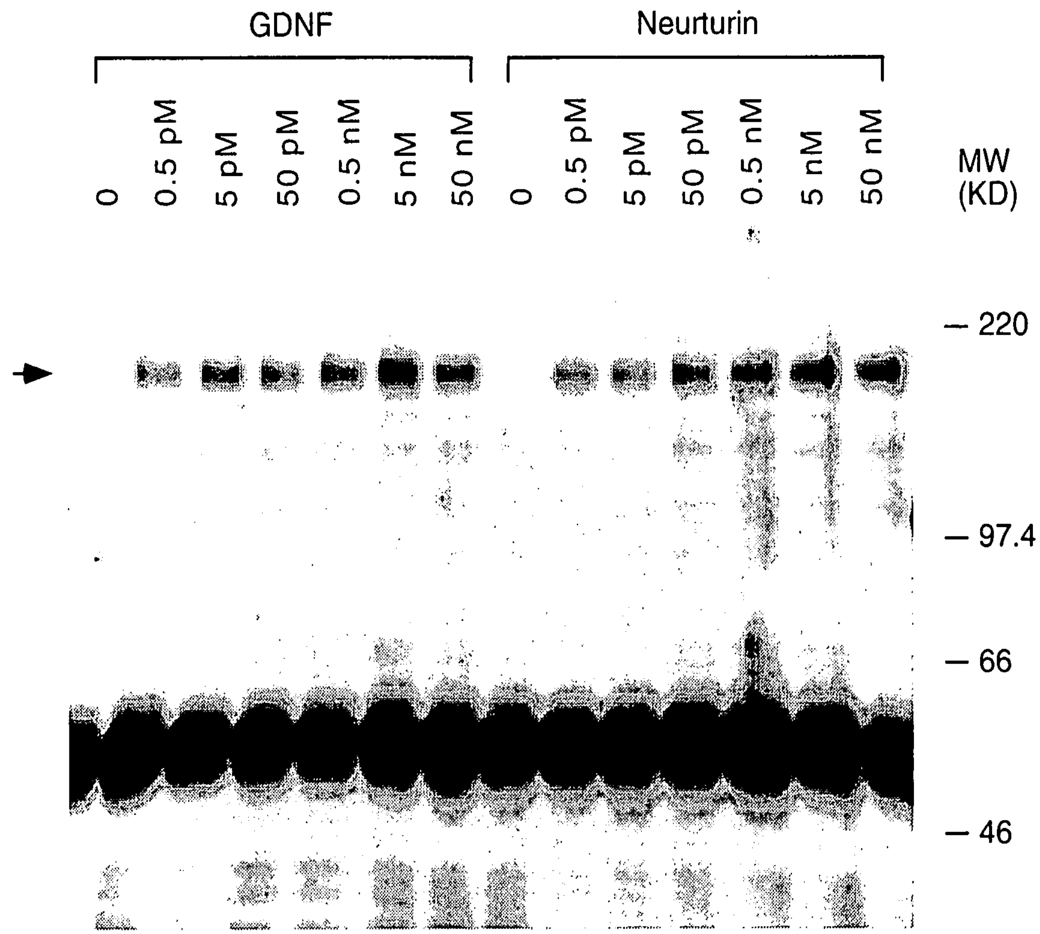

GDNF
Neurturin
0
0.5 pM
5 pM
50 pM
0.5 nM
5 nM
50 nM
0
0.5 pM
5 pM
50 pM
0.5 nM
5 nM
50 nM
MW
(KD)
— 220
— 97.4
— 66
— 46

Figure 25

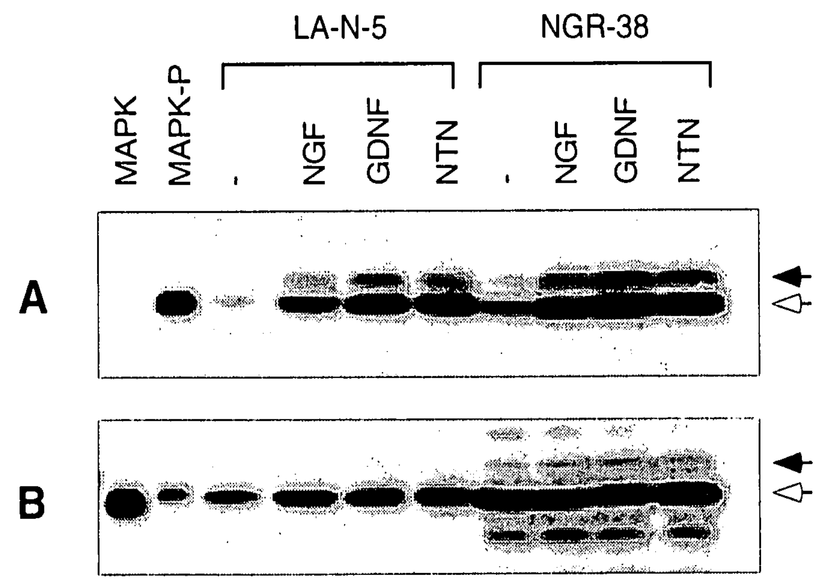


Figure 26

```
              1                                                    50
CONSENSUS     .........P ....l.tl.s l..pl.l..S .....r...d Cv.A...C.a
GDNFR         .......... ..MFLATLYF ALPLLDLLMS AEVSGGDRLD CVKASDQCLK
GRR2          .....MLVFP SHYPDETLRS LASPSSLQGS ELHGWRPQVD CVRANELCAA
GRR3          MGLSRSPRPP PLVILLLVLS LWLPLGTGNS LPTENRLVNS CTQARKKCEA

              51                                                  100
CONSENSUS     e..Cs..Yrt LrqC.ag... n........a ..eC..A.e. L..ssLydCR
GDNFR         EQSCSTKYRT LRQCVAGKET NFSLTSGLEA KDECRSAMEA LKQKSLYNCR
GRR2          ESNCSSRYRT LRQCLAGRDR N.....TMLA NKECQAALEV LQESPLYDCR
GRR3          NPACKAAYQH LDSCTPSLSS PLPSGES.AT SAACLEAAQQ LRNSSLIDCR

              101                                                 150
CONSENSUS     CkRgMKke.. CL.IYWs.h. .l..G...le .SPYE.pVtS rlsdifr..s
GDNFR         CKRGMKKEKN CLRIYWSMYQ SL.QGNDLLE DSPYE.PVNS RLSDIFRAVP
GRR2          CKRGMKKELQ CLQIYWSIHL GLTEGEEFYE ASPYE.PVTS RLSDIFRLAS
GRR3          CHRRMKHQAT CLDIYWTVHP VRSLGDYELD VSPYEDTVTS ..KPWKMNLS

              151                                                 200
CONSENSUS     ..S....d.. ...ksn.CLd aAkaCnLnD. CkklRsaYi. .C....S..e
GDNFR         FISDVFQQVE HISKGNNCLD AAKACNLDDT CKKYRSAYIT PCTTSMS.NE
GRR2          IFSGTGTDPA VSTKSNHCLD AAKACNLNDN CKKLRSSYIS ICNREISPTE
GRR3          KLSMLKPD.. ....SDLCLK FAMLCTLNDK CDRLRKAYGE AC....SG.I

              201                                                 250
CONSENSUS     rCnRrkChka LRqFFdkvp. .h.ygmLfCs C...D.aC.E RRRqTI.PsC
GDNFR         VCNRRKCHKA LRQFFDKVPA KHSYGMLFCS C..RDIACTE RRRQTIVPVC
GRR2          RCNRRKCHKA LRQFFDRVPS EYTYRMLFCS C..QDQACAE RRRQTILPSC
GRR3          RCQRHLCLAQ LRSFFEKAAE SHAQGLLLCP CAPEDAGCGE RRRNTIAPSC

              251                                                 300
CONSENSUS     sye..e.PNC LdLrs.Crtd .lCRSRLaDF .tnC.p..r. .t.C.a.ny.
GDNFR         SYEERERPNC LSLQDSCKTN YICRSRLADF FTNCQPESRS VSNCLKENYA
GRR2          SYEDKEKPNC LDLRSLCRTD HLCRSRLADF HANCRASYRT ITSCPADNYQ
GRR3          ALPSVA.PNC LDLRSFCRAD PLCRSRLMDF QTHCHPMDIL GT.C.ATEQS

              301                                                 350
CONSENSUS     .CL.aY.GlI Gt.MTPNyvd s..t...Vap wC.CrgSGN. .eeCekfl..
GDNFR         DCLLAYSGLI GTVMTPNYVD SSSL..SVAP WCDCSNSGND LEDCLKFLNF
GRR2          ACLGSYAGMI GFDMTPNYVD SNPTGIVVSP WCNCRGSGNM EEECEKFLRD
GRR3          RCLRAYLGLI GTAMTPNFIS KVNTT..VAL GCTCRGSGNL QDECEQLEKS

              351                                                 400
CONSENSUS     F..NpCL.nA IqAfgng.dv .msq..p... .t.a...... rv...p.l..
GDNFR         FKDNTCLKNA IQAFGNGSDV TMWQPAPPVQ TTTATTTTAF RVKNKP.LGP
GRR2          FTENPCLRNA IQAFGNGTDV NMSPKGPSLP ATQAP..... RVEKTPSLPD
GRR3          FSQNPCLMEA IAAKMRFHRQ LFSQDWADST FSVMQQQNSS PALRPQ....

              401                                                 450
CONSENSUS     ..s......t .v...c...q .q.lk.n.s. ....c..... ..........
GDNFR         AGS.ENEIPT HVLPPCANLQ AQKLKSNVSG STHLCLSDSD FGKDGLAGAS
GRR2          DLSDSTSLGT SVITTCTSIQ EQGLKANNSK ELSMCFTELT TNISPGSKKV
GRR3          .......... .......... .......... .......... ..........

              451                                     489
CONSENSUS     ......s..a ..s..l..LP vLmlt.l... l...l.ets
GDNFR         SHITTKSMAA PPSCSLSSLP VLMLTALAAL LSVSLAETS
GRR2          IKLNSGSSRA RLSAALTALP LLMLTLAL
GRR3          .......... ......LRLP VLSFFILTLI LLQTLW
```